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=> s neocentromere
L1 196 NEOCENTROMERE

=> s l1 and (HAC or MAC or YAC or PAC or BAC)
L2 18 L1 AND (HAC OR MAC OR YAC OR PAC OR BAC)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 9 DUP REM L2 (9 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L3 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:546578 CAPLUS
DN 141:83550
TI Genetic therapy and genetic modification using neocentromeric minichromosomes
IN Choo, Andy; Saffery, Richard Eric; Wong, Lee Hwa
PA Murdoch Childrens Research Institute, Australia
SO PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004057006	A1	20040708	WO 2003-AU1723	20031223

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI AU 2002-953516 A 20021223
AB The present invention provides a target region within a mammalian, avian, plant or other eukaryotic chromosome or an artificial or engineered chromosomal construct which is capable of carrying and expressing a heterologous gene or other genetic mol. of interest. The gene or genetic mol. of interest is expressed in a region of the chromosome which corresponds to or which immediately adjoins or is proximal to a centromeric or neocentromeric region or a functional deriv. thereof or a latent, synthetic or hybrid form thereof. A method for facilitating genetic therapy or genetic modification or other applications are also provided including protein prodn. for proteomic therapy in a mammal, avian species or plant or other higher eukaryotes.

L3 ANSWER 2 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 1
AN 2003:536224 BIOSIS
DN PREV200300524122
TI Genomic microarray analysis reveals distinct locations for the CENP-A binding domains in three human chromosome 13q32 neocentromeres.
AU Alonso, Alicia; Mahmood, Radma; Li, Shulan; Cheung, Fanny; Yoda, Kinya; Warburton, Peter E. [Reprint Author]
CS Department of Human Genetics, Mount Sinai School of Medicine, 1425 Madison
Ave, East Bldg 14-52A, Box 1498, New York, NY, 10029, USA
peter.warburton@mssm.edu
SO Human Molecular Genetics, (15 October 2003) Vol. 12, No. 20, pp. 2711-2721. print.
ISSN: 0964-6906 (ISSN print).
DT Article
LA English
ED Entered STN: 12 Nov 2003
Last Updated on STN: 12 Nov 2003
AB Human neocentromeres are fully functional centromeres that provide mitotic stability to rearranged chromosomes that have separated from endogenous centromeres. A disproportionate number of neocentromeres has been observed in certain regions such as chromosome 3q (n=6), 15q (n=9) and 13q32 (n=7), suggesting that these regions contain DNA sequences with a high propensity for ***neocentromere*** formation. Therefore, we have addressed the role of primary DNA sequence in ***neocentromere*** formation by asking whether multiple independent neocentromeres that were cytologically localized to chromosome 13q32 are in fact localized to the same underlying genomic DNA. Analysis of four independent 13q32 neocentromeres using simultaneous FISH with ordered ***YAC*** probes and immunofluorescence with antibodies to CENP-C have localized three neocentromeres to a distal apprx7 Mb domain in chromosome 13q32, and one to an overlapping proximal domain of apprx7 Mb. DNA was obtained from three of these neocentromeres by CENP-A chromatin immunoprecipitation (ChIP) and used to screen ordered BACs using both a slot-blotted ***BAC*** pool approach and a genomic microarray that contiguously spans 13q31.3-13q33.1. The CENP-A binding domains from each of these neocentromeres was identified to distinct genomic locations of apprx130, 215 and 275 kb within an apprx6.5 Mb region. Thus, the lack of

coincidence of these neocentromeres to the same underlying DNA sequence refutes the idea of a DNA sequence based ***neocentromere*** 'hotspot' in 13q32 and further supports the sequence-independent epigenetic formation of human neocentromeres. The screening of genomic microarrays with ChIP DNA provides a powerful method to identify mammalian DNA sequences associated with particular functional chromatin states.

L3 ANSWER 3 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 2
AN 2003:427714 BIOSIS
DN PREV200300427714
TI A rapid method of genomic array analysis of scaffold/matrix attachment regions (S/MARs) identifies a 2.5-Mb region of enhanced scaffold/matrix attachment at a human ***neocentromere*** .
AU Sumer, Huseyin; Craig, Jeffrey M.; Sibson, Mandy; Choo, K. H. Andy [Reprint Author]
CS Murdoch Childrens Research Institute, Royal Children's Hospital, Melbourne, Victoria, 3052, Australia
choo@cryptic.rch.unimelb.edu.au
SO Genome Research, (July 2003) Vol. 13, No. 7, pp. 1737-1743. print.
ISSN: 1088-9051 (ISSN print).
DT Article
LA English
ED Entered STN: 17 Sep 2003
Last Updated on STN: 17 Sep 2003
AB Human neocentromeres are fully functional centromeres that arise at previously noncentromeric regions of the genome. We have tested a rapid procedure of genomic array analysis of chromosome scaffold/matrix attachment regions (S/MARs), involving the isolation of S/MAR DNA and hybridization of this DNA to a genomic ***BAC*** / ***PAC*** array. Using this procedure, we have defined a 2.5-Mb domain of S/MAR-enriched chromatin that fully encompasses a previously mapped centromere protein-A (CENP-A)-associated domain at a human ***neocentromere*** . We have independently verified this procedure using a previously established fluorescence in situ hybridization method on salt-treated metaphase chromosomes. In silico sequence analysis of the S/MAR-enriched and surrounding regions has revealed no outstanding sequence-related predisposition. This study defines the S/MAR-enriched domain of a higher eukaryotic centromere and provides a method that has broad application for the mapping of S/MAR attachment sites over large genomic regions or throughout a genome.

L3 ANSWER 4 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 3
AN 2003:502083 BIOSIS
DN PREV200300504012
TI Chromosome 6 phylogeny in primates and centromere repositioning.
AU Eder, Verena [Reprint Author]; Ventura, Mario [Reprint Author]; Ianigro, Massimo; Teti, Mariagrazia [Reprint Author]; Rocchi, Mariano [Reprint Author]; Archidiacono, Nicoletta [Reprint Author]
CS Sezione di Genetica, DAPEG, Bari, Italy
archidiacono@biologia.uniba.it
SO Molecular Biology and Evolution, (September 2003) Vol. 20, No. 9, pp. 1506-1512. print.
CODEN: MBEVEO. ISSN: 0737-4038.
DT Article
LA English
ED Entered STN: 29 Oct 2003
Last Updated on STN: 29 Oct 2003
AB A panel of 15 human ***BAC*** / ***PAC*** probes, covering the entire chromosome 6, was used in FISH experiments on great apes and on representatives of Old World monkeys, New World monkeys, and lemurs to delineate the chromosome 6 phylogeny in primates. The domestic cat was used as an outgroup. The analysis showed a high marker order conservation, with few rearrangements required to reconcile the hypothesized chromosome 6 organization in primate ancestor with marker arrangement in all the examined species. Contrary to this simple evolutionary scenario, however, the centromere was found to be located in three distinct regions, without any evidence of chromosomal rearrangement that would account for its movement. One of the two centromere repositioning events occurred in great apes ancestor. The centromere moved from 6p22.1 to the present day location after the inversion event that differentiated marker order of the primate ancestor from the ancestor of Catarrhini. A cluster of intrachromosomal segmental duplications was found at 6p22.1, scattered in a region of about 9 Mb, which we interpret as remains of duplicons that flanked the ancestral centromere. Our data, therefore, suggest that some duplicon clusters found in noncentromeric/nontelomeric locations may represent traces of evolutionary silenced centromeres that inactivated after the occurrence of a centromere repositioning. In addition, the ***neocentromere*** emergence we have documented in Old World monkeys at 6q24.3 appears to have arisen and progressed without affecting the displaced flanking sequences.

L3 ANSWER 5 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 4
AN 2004:241195 BIOSIS
DN PREV200400245701
TI Chromosome homology between chicken (Gallus gallus domesticus) and the red-legged partridge (Alectoris rufa): evidence of the occurrence of a ***neocentromere*** during evolution.
AU Kasai, F.; Garcia, C.; Arruga, M. V.; Ferguson-Smith, M. A. [Reprint Author]
CS Cambridge University Centre for Veterinary Science, Madingley Road, Cambridge, CB3 0ES, UK
maf12@mole.bio.cam.ac.uk
SO Cytogenetic and Genome Research, (2003) Vol. 102, No. 1-4, pp. 326-330. print.
ISSN: 1424-8581 (ISSN print).
DT Article
LA English
ED Entered STN: 6 May 2004
Last Updated on STN: 6 May 2004
AB Chromosome-specific paints from macrochromosomes 1-9 and Z of the chicken
were hybridised to metaphases of the red-legged partridge and revealed no inter-chromosomal rearrangements. The results from chromosome painting are similar to previous studies on the Japanese quail but different from findings in guinea fowl and several species of pheasant. The difference in centromere position in chicken and partridge chromosome 4, previously assumed to be the result of an inversion, was confirmed. However, FISH mapping of ***BAC*** clones from chicken chromosome 4 revealed that the order of loci was the same in both species, indicating the occurrence of a ***neocentromere*** during divergence.

L3 ANSWER 6 OF 9 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN
AN 2003116796 EMBASE
TI Prenatal diagnosis of a karyotypically normal pregnancy in a mother with a supernumerary neocentric 13q21 .fwdarw. 13q22 chromosome and balancing reciprocal deletion.
AU Knegt A.C.; Li S.; Engelen J.J.M.; Bijlsma E.K.; Warburton P.E.
CS P.E. Warburton, Department of Human Genetics, Box 1498, Mount Sinai School
of Medicine, 1425 Madison Ave, New York, NY 10029, United States.
peter.warburton@mssm.edu
SO Prenatal Diagnosis, (1 Mar 2003) 23/3 (215-220).
Refs: 17
ISSN: 0197-3851 CODEN: PRDIDM
CY United Kingdom
DT Journal; Article
FS 007 Pediatrics and Pediatric Surgery
022 Human Genetics
LA English
SL English
AB An adult female patient with a history of miscarriages was found to be carrying a stable supernumerary chromosome. The patient also carried a reciprocal paracentric deletion in chromosome 13q21/22. Microdissection and reverse fluorescence in situ hybridization FISH revealed that this supernumerary chromosome was derived from region 13q21 .fwdarw. 13q22. The
presence of a ***neocentromere*** on this supernumerary chromosome was confirmed by the absence of detectable alpha satellite DNA using FISH and the presence of centromere proteins CENP-C and CENP-A using immunofluorescence. The absence of telomere sequences suggests that the marker is a ring chromosome (r(13)). FISH using ordered BACs from the chromosome region 13q21 .fwdarw. 13q31 permitted the precise positioning of the r(13) chromosome and the corresponding deletion to chromosome bands 13q21.32 .fwdarw. 13q22.2. ***BAC*** 280J7 from within the r(13) was used as a FISH probe for the prenatal analysis of amniocytes at 16 weeks of gestation, which revealed a normal karyotype for the fetus. This r(13) chromosome represents the first description of chromosome 13 of the rarer class of neocentric chromosomes that are derived from interstitial deletions. It represents the first example of prenatal diagnosis in a phenotypically normal female that was ascertained to carry a neocentric marker. The presence of such a neocentric marker/deletion karyotype in a parent presents unique possible karyotypic outcomes for conceptions and unusual challenges for genetic counseling. Copyright .COPYRGT. 2003 John Wiley & Sons, Ltd.

L3 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:487757 CAPLUS
DN 137:42666
TI ***Neocentromere*** -based human minichromosome construction by telomere-associated chromosomal truncation
IN Choo, Kong-Hong Andy; Wong, Lee Hwa; Saffery, Richard Eric
PA Amrad Operations Pty Ltd, Australia; Murdoch Childrens Research Institute
SO PCT Int. Appl., 61 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002050288	A1	20020627	WO 2001-AU1644	20011220
WO 2002050288	C2	20030807		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PI AU 2002015697 A5 20020701 AU 2002-15697 20011220
EP 1354055 A1 20031022 EP 2001-271443 20011220
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
JP 2004525615 T2 20040826 JP 2002-552165 20011220
US 2004081982 A1 20040429 US 2003-463981 20030617
PRAI AU 2000-2247 A 20001221
AU 2001-8909 A 20011116
WO 2001-AU1644 W 20011220
AB The present invention is directed generally to a defined or isolated nucleic acid mol. encompassing a neocentreomere or a functional deriv. thereof or a latent, synthetic or hybrid form thereof and its use inter alia in developing a range of eukaryotic mini-chromosomes and artificial chromosomes including mammalian (e.g. human) and non-mammalian mini-chromosomes and artificial chromosomes. The present invention further provides a telomere-assocd. chromosome truncation (TACT) approach to develop mini-chromosomes, but is not limited to this approach. It is directed to any truncation approach that produces a ***neocentromere*** -contg. mini-chromosome, or any transfection approach using cloned or pre-fabricated DNA that provides ***neocentromere*** function in the construction of artificial chromosome. Such mini-chromosomes and artificial chromosomes are useful in a range of genetic therapies. Neocentromeres (NCs) are fully functional centromeres that arise ectopically in noncentromeric regions lacking .alpha.-satellite DNA. Using telomere-assocd. chromosome truncation, the inventors have produced a series of minichromosomes (MiCs) from a mardel(10) marker chromosome contg. a previously characterized human NC. These MiCs range in size from .apprxeq.0.7 to 1.8 Mb and contain single-copy intact genomic DNA from the 10q25 region. Two of these NC-based Mi-Cs (NC-MiCs) appear circular whereas one is linear. All demonstrate stability in both structure and mitotic transmission in the absence of drug selection. Presence of a functional NC is shown by binding a host of key centromere-assocd. proteins. These NC-MiCs provide direct evidence for mitotic segregation function of the NC DNA and represent examples of stable mammalian MiCs lacking centromeric repeats.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 8 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 5
AN 2002:271810 BIOSIS
DN PREV200200271810
TI Cytogenetic analysis and construction of a ***BAC*** contig across a common neocentromeric region from 9p.
AU Satinover, D. L.; Vance, G. H.; Van Dyke, D. L.; Schwartz, S. [Reprint author]
CS Department of Genetics and Center for Human Genetics, Case Western Reserve University School of Medicine and University Hospitals Cleveland, Cleveland, OH, 44106-9959, USA
sxs95@po.cwru.edu
SO Chromosoma (Berlin), (August, 2001) Vol. 110, No. 4, pp. 275-283. print. CODEN: CHROAU. ISSN: 0009-5915.
DT Article
LA English
ED Entered STN: 1 May 2002
Last Updated on STN: 1 May 2002
AB Over 40 cases of neocentric marker chromosomes, without detectable alpha-satellite DNA, have been reported. Although these have originated from many different chromosomes, a few of these chromosomes have been involved in multiple cases of marker formation. In this study, two different markers originating from the short arm of chromosome 9 were analyzed, identifying a common neocentromeric region. A bacterial artificial chromosome (***BAC***) contig extending over more than 900 kb has been assembled across this neocentromeric region. Fluorescent in situ hybridization and immunofluorescence assays (CENP-C and CENP-E) have localized the ***neocentromere*** to a 500 kb region. Preliminary analysis of DNA sequences in this ***neocentromere*** revealed a highly AT-rich region, which also has an increase in the level of retroviral elements compared with the average levels in the genome.

L3 ANSWER 9 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:181699 CAPLUS
DN 128:304528
TI Direct cloning of human 10q25 ***neocentromere*** DNA using transformation-associated recombination (TAR) in yeast
AU Cancilla, Michael R.; Tainton, Kellie M.; Barry, Alyssa E.; Larionov, Vladimir; Kouprina, Natalya; Resnick, Michael A.; Du Sart, Desiree; Choo, K. H. Andy
CS Murdoch Institute Research Birth Defects, Royal Children's Hospital, Parkville, 3052, Australia
SO Genomics (1998), 47(3), 399-404
CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB The transformation-assocd. recombination (TAR) procedure allows rapid, site-directed cloning of specific human chromosomal regions as yeast artificial chromosomes (YACs). The procedure requires knowledge of only a single, relatively small genomic sequence that resides adjacent to the chromosomal region of interest. We applied this approach to the cloning of the ***neocentromere*** DNA of a marker chromosome that we have previously shown to have originated through the activation of a latent centromere at human chromosome 10q25. Using a unique 1.4-kb DNA fragment as a "hook" in TAR expts., we achieved single-step isolation of the crit. ***neocentromere*** DNA region as two stable, 110- and 80-kb circular YACs. For obtaining large quantities of highly purified DNA, these YACs were retrofitted with the yeast-bacteria-mammalian-cells shuttle vector BRV1, electroporated into Escherichia coli DH10B, and isolated as bacterial artificial chromosomes (BACs). Extensive characterization of these YACs and BACs by PCR and restriction analyses revealed that they are identical to the corresponding regions of the normal chromosome 10 and provided further support for the formation of the ***neocentromere*** within the marker chromosome through epigenetic activation.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s l1 and chromosome 10
L4 30 L1 AND CHROMOSOME 10

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5 17 DUP REM L4 (13 DUPLICATES REMOVED)

=> s l5 not l3
L6 17 L5 NOT L3

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 17 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:569102 BIOSIS
DN PREV200300569599
TI Distribution of retroelements in centromeres and neocentromeres of maize.
AU Mroczek, Rebecca J.; Dawe, R. Kelly [Reprint Author]
CS Department of Plant Biology, University of Georgia, Miller Plant Sciences Bldg., Athens, GA, 30602, USA
kelly@dogwood.botany.uga.edu
SO Genetics, (October 2003) Vol. 165, No. 2, pp. 809-819. print. ISSN: 0016-6731 (ISSN print).
DT Article
LA English
ED Entered STN: 3 Dec 2003
Last Updated on STN: 3 Dec 2003
AB Fluorescent in situ hybridization was used to examine the distribution of six abundant long terminal repeat (LTR) retroelements, Opie, Huck, Cinful-1, Prem-2/Ji, Grande, and Tekay/Prem-1 on maize pachytene chromosomes. Retroelement staining in euchromatin was remarkably uniform, even when we included the structurally polymorphic abnormal ***chromosome*** ***10*** (Ab10) in our analysis. This uniformity made it possible to use euchromatin as a control for quantitative staining intensity measurements in other regions of the genome. The data show that knobs, known to function as facultative neocentromeres when Ab10 is present, tend to exclude retroelements. A notable exception is Cinful-1, which accumulates in TR-1 knob arrays. Staining for each of the six retroelements was also substantially reduced in centromeric satellite arrays to an average of 30% of the staining in euchromatin. This contrasted with two previously described centromere-specific retrotransposable (CR) elements that were readily detected in centromeres. We suggest that retroelements are relatively rare in centromeres because they interrupt the long satellite arrays thought to be required for efficient centromere function. CR elements may have evolved mutualistic relationships with their plant hosts: they are known to interact with the kinetochore protein CENH3 and appear to accumulate in clusters, leaving long satellite arrays intact.

L6 ANSWER 2 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 2003:425262 BIOSIS
DN PREV200300425262
TI Four loci on abnormal ***chromosome*** ***10*** contribute to meiotic drive in maize.
AU Hiatt, Evelyn N.; Dawe, R. Kelly [Reprint Author]
CS Department of Plant Biology, University of Georgia, Miller Plant Sciences Bldg., Athens, GA, 30602, USA
kelly@dogwood.botany.uga.edu
SO Genetics, (June 2003) Vol. 164, No. 2, pp. 699-709. print. ISSN: 0016-6731 (ISSN print).
DT Article
LA English
ED Entered STN: 17 Sep 2003
Last Updated on STN: 17 Sep 2003
AB We provide a genetic analysis of the meiotic drive system on maize abnormal ***chromosome*** ***10*** (Ab10) that causes preferential segregation of specific chromosomal regions to the reproductive megaspore.

The data indicate that at least four chromosomal regions contribute to meiotic drive, each providing distinct functions that can be differentiated from each other genetically and/or phenotypically. Previous reports established that meiotic drive requires ***neocentromere*** activity at specific tandem repeat arrays (knobs) and that two regions on Ab10 are involved in trans-activating neocentromeres. Here we confirm and extend data suggesting that only one of the ***neocentromere*** -activating regions is sufficient to move many knobs. We also confirm the localization of a locus/loci on Ab10, thought to be a prerequisite for meiotic drive, which promotes recombination in structural heterozygotes. In addition, we identified two new and independent functions required for meiotic drive. One was identified through the characterization of a deletion derivative of Ab10 (Df(L)) and another as a newly identified meiotic drive mutation (suppressor of meiotic drive 3). In the absence of either function, meiotic drive is abolished but ***neocentromere*** activity and the recombination effect typical of Ab10 are unaffected. These results demonstrate that ***neocentromere*** activity and increased recombination are not the only events required for meiotic drive.

L6 ANSWER 3 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2002:329478 BIOSIS
DN PREV200200329478
TI Construction of ***neocentromere*** -based human minichromosomes for gene delivery and centromere studies.
AU Wong, L. H.; Saffery, R.; Choo, K. H. A. [Reprint author]
CS Murdoch Childrens Research Institute, Royal Children's Hospital, Flemington Road, Melbourne, VIC, 3052, Australia
SO Gene Therapy, (June, 2002) Vol. 9, No. 11, pp. 724-726 print. ISSN: 0969-7128.
DT Article
LA English
ED Entered STN: 12 Jun 2002
Last Updated on STN: 12 Jun 2002
AB Human neocentromeres are fully functional centromeres that arise naturally in non-centromeric regions devoid of alpha-satellite DNA. We have successfully produced a series of minichromosomes by telomere-associated truncation of a marker chromosome mardel(10) containing a ***neocentromere*** . The resulting minichromosomes are either linear or circular in nature, and range in size from approximately 650 kb to 2 Mb. These minichromosomes exhibit full centromeric activity, bind to essential centromere proteins, and are mitotically stable over many generations. They provide a useful system for dissecting the functional domains of complex eukaryotic centromeres and as vectors for therapeutic gene delivery.

L6 ANSWER 4 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2002:241597 BIOSIS
DN PREV200200241597
TI Independently regulated ***neocentromere*** activity of two classes of tandem repeat arrays.
AU Hiatt, Evelyn N.; Kentner, Edward K.; Dawe, R. Kelly [Reprint author]
CS Department of Genetics, University of Georgia, Athens, GA, 30602, USA kelly@dogwood.botany.uga.edu
SO Plant Cell, (February, 2002) Vol. 14, No. 2, pp. 407-420. print. CODEN: PLCEEW. ISSN: 1040-4651.
DT Article
LA English
ED Entered STN: 17 Apr 2002
Last Updated on STN: 17 Apr 2002
AB Tandem repeat arrays often are found in interstitial (i.e., normally gene-rich) regions on chromosomes. In maize, genes on abnormal ***chromosome*** ***10*** induce the tandem repeats that make up knobs to move poleward on the meiotic spindle. This so-called ***neocentromere*** activity results in the preferential recovery, or meiotic drive, of the knobs in progeny. Here we show that two classes of repeats differ in their capacity to form neocentromeres and that their motility is controlled in trans by at least two repeat-specific activators. Microtubule dynamics appear to contribute little to the movement of neocentromeres (they are active in the presence of taxol), suggesting that the mechanism of motility involves microtubule-based motors. These data suggest that maize knob repeats and their binding proteins have coevolved to ensure their preferential recovery in progeny. ***Neocentromere*** -mediated drive provides a plausible mechanism for the evolution and maintenance of repeat arrays that occur in interstitial positions.

L6 ANSWER 5 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2001:266965 BIOSIS
DN PREV200100266965
TI A 330 kb CENP-A binding domain and altered replication timing at a human ***neocentromere*** .
AU Lo, Anthony W. I.; Craig, Jeffrey M.; Saffery, Richard; Kalitsis, Paul; Irvine, Danielle V.; Earle, Elizabeth; Magliano, Dianna J.; Choo, K. H. Andy [Reprint author]
CS The Murdoch Childrens Research Institute, Royal Children's Hospital, Flemington Road, Melbourne, Victoria, 3052, Australia
choo@cryptic.rch.unimelb.edu.au
SO EMBO (European Molecular Biology Organization) Journal, (April 17, 2001) Vol. 20, No. 8, pp. 2087-2096. print. CODEN: EMJODG. ISSN: 0261-4189.
DT Article
LA English
ED Entered STN: 6 Jun 2001
Last Updated on STN: 19 Feb 2002
AB Centromere protein A (CENP-A) is an essential centromere-specific histone H3 homologue. Using combined chromatin immunoprecipitation and DNA array analysis, we have defined a 330 kb CENP-A binding domain of a 10q25.3 ***neocentromere*** found on the human marker chromosome mardel(10). This domain is situated adjacent to the 80 kb region identified previously as the ***neocentromere*** site through lower-resolution immunofluorescence/FISH analysis of metaphase chromosomes. The 330 kb CENP-A binding domain shows a depletion of histone H3, providing evidence for the replacement of histone H3 by CENP-A within centromere-specific nucleosomes. The DNA within this domain has a high AT-content comparable to that of alpha-satellite, a high prevalence of LINEs and tandem repeats, and fewer SINEs and potential genes than the surrounding region. FISH analysis indicates that the normal 10q25.3 genomic region replicates around mid-S phase. ***Neocentromere*** formation is accompanied by a replication time lag around but not within the CENP-A binding region, with this lag being significantly more prominent to one side. The availability of fully sequenced genomic markers makes human neocentromeres a powerful model for dissecting the functional domains of complex higher eukaryotic centromeres.

L6 ANSWER 6 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2001:173170 BIOSIS
DN PREV200100173170
TI Prenatal molecular cytogenetic diagnosis of partial tetrasomy 10p due to ***neocentromere*** formation in an inversion duplication analphoid marker chromosome.
AU Levy, B. [Reprint author]; Papenhausen, P. R.; Tepperberg, J. H.; Dunn, T. M.; Fallet, S.; Magid, M. S.; Kardon, N. B.; Hirschhorn, K.; Warburton, P. E.
CS Department of Human Genetics, Mount Sinai School of Medicine, One Gustave
L. Levy Place, New York, NY, 10029, USA
brynn.levy@mssm.edu
SO Cytogenetics and Cell Genetics, (2000 (2001)) Vol. 91, No. 1-4, pp. 165-170. print. CODEN: CGCGBR. ISSN: 0301-0171.
DT Article
LA English
ED Entered STN: 11 Apr 2001
Last Updated on STN: 18 Feb 2002
AB Neocentromeres are fully functional centromeres found on rearranged or marker chromosomes that have separated from endogenous centromeres. Neocentromeres often result in partial tri- or tetrasomy because their formation confers mitotic stability to acentric chromosome fragments that would normally be lost. We describe the prenatal identification and characterization of a de novo supernumerary marker chromosome (SMC) containing a ***neocentromere*** in a 20-wk fetus by the combined use of comparative genomic hybridization (CGH) and fluorescence in situ hybridization (FISH). GTG-banding of fetal metaphases revealed a 47,XY,+mar karyotype in 100% of cultured amniocytes; parental karyotypes were both normal. Although sequential tricolor FISH using chromosome-specific painting probes identified a ***chromosome*** ***10*** origin of the marker, a complete panel of chromosome-specific centromeric satellite DNA probes failed to hybridize to any portion of the marker. The presence of a ***neocentromere*** on the marker chromosome was confirmed by the absence of hybridization of an all-human-centromere alpha-satellite DNA probe, which hybridizes to all normal centromeres, and the presence of centromere protein (CENP)-C, which is associated specifically with active kinetochores. Based on CGH analysis and FISH with a chromosome 10p subtelomeric probe, the marker was found to be an inversion duplication of the distal portion of chromosome 10p. Thus, the proband's karyotype was 47,XY,+inv dup(10)(pter fwdarw p14 apprx 15::p14 apprx 15 fwdarw neo fwdarw pter), which is the first report of partial tetrasomy 10p resulting from an analphoid marker chromosome with a ***neocentromere*** . This study illustrates the use of several molecular strategies in distinguishing centric alphoid markers from neocentric analphoid markers.

L6 ANSWER 7 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2000:381305 BIOSIS
DN PREV200000381305
TI The 10q25 ***neocentromere*** and its inactive progenitor have identical primary nucleotide sequence: Further evidence for epigenetic modification.
AU Barry, Alyssa E.; Bateman, Melissa; Howman, Emily V.; Cancilla, Michael R.; Tainton, Kellie M.; Irvine, Danielle V.; Saffery, Richard; Choo, K. H. Andy [Reprint author]
CS Murdoch Childrens Research Institute, Royal Children's Hospital, Parkville, 3052, Australia
SO Genome Research, (June, 2000) Vol. 10, No. 6, pp. 832-838. print. ISSN: 1088-9051.

DT Article
LA English
ED Entered STN: 6 Sep 2000
Last Updated on STN: 8 Jan 2002
AB We have previously localized the core centromere protein-binding domain of a 10q25.2-derived ***neocentromere*** to an 80-kb genomic region. Detailed analysis has indicated that the 80-kb ***neocentromere*** (NC) DNA has a similar overall organization to the corresponding region on a normal ***chromosome*** ***10*** (HC) DNA, derived from a genetically unrelated CEPH individual. Here we report sequencing of the HC DNA and its comparison to the NC sequence. Single-base differences were observed at a maximum rate of 4.6 per kb; however, no deletions, insertions, or other structural rearrangements were detected. To investigate whether the observed changes, or subsets of these, might be de novo mutations involved in neocentromerization (i.e., in committing a region of a chromosome to ***neocentromere*** formation), the progenitor DNA (PnC) from which the NC DNA descended, was cloned and sequenced. Direct comparison of the PnC and NC sequences revealed 100% identity, suggesting that the differences between NC and HC DNA are single nucleotide polymorphisms (SNPs) and that formation of the 10q25.2 NC did not involve a change in DNA sequence in the core centromere protein-binding NC region. This is the first study in which a cloned NC DNA has been compared directly with its inactive progenitor DNA at the primary sequence level. The results form the basis for future sequence comparison outside the core protein-binding domain, and provide direct support for the involvement of an epigenetic mechanism in neocentromerization.

L6 ANSWER 8 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1999:299673 BIOSIS
DN PREV199900299673
TI Sequence and analysis of a human ***neocentromere*** .
AU Barry, Alyssa E. [Reprint author]; Howman, Emily V. [Reprint author]; Cancilla, Michael R. [Reprint author]; Saffery, Richard [Reprint author]; Choo, K. H. Andy [Reprint author]
CS Murdoch Institute, Royal Childrens Hospital, Flemington Rd, 10th Floor, Parkville, VIC, Australia
SO FASEB Journal, (April 23, 1999) Vol. 13, No. 7, pp. A1375. print.
Meeting Info.: Annual Meeting of the American Societies for Experimental Biology on Biochemistry and Molecular Biology 99. San Francisco, California, USA. May 16-20, 1999. American Societies for Experimental Biology.
CODEN: FAJOEC. ISSN: 0892-6638.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Aug 1999
Last Updated on STN: 12 Aug 1999

L6 ANSWER 9 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1999:135522 BIOSIS
DN PREV199900135522
TI Sequence analysis of an 80 kb human ***neocentromere*** .
AU Barry, Alyssa E.; Howman, Emily V.; Cancilla, Michael R ; Saffery, Richard; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst., Royal Children's Hosp., Flemington Road, Parkville 3052, Australia
SO Human Molecular Genetics, (Feb., 1999) Vol. 8, No. 2, pp. 217-227. print.
ISSN: 0964-6906.
DT Article
LA English
ED Entered STN: 31 Mar 1999
Last Updated on STN: 31 Mar 1999
AB We previously described the cloning of an 80 kb DNA corresponding to the core protein-binding domain of a human ***chromosome*** ***10*** -derived ***neocentromere*** . Here we report the complete sequence of this DNA (designated NC DNA) and its detailed structural analysis. The sequence is devoid of human centromeric alpha-satellite DNA and the pericentric beta- and gamma-satellites, the ATRS and 48 bp repeat DNA. One copy of a sequence that is related to the CENPB box motif is present, and a number of copies of other pericentric sequences including pJa and classical satellites I and III are present but both their relative sparsity and non-tandem organization suggest that each sequence, on its own, is unlikely to mimic any role the sequence may have in the normal centromere. The DNA-binding motifs of the architectural and regulatory proteins HMGI and topoII have a normal abundance and random distribution, implying that these sequences are not key functional elements. The total A + T content of the sequence is not notably different from that of the human genome, but an abundance of AT-rich islands and a biased distribution of these islands within the NC sequence are clearly discernible and may be functionally significant. Substantial amounts of transposable elements and low copy number tandem repeats, including several that are highly AT- and purine-rich, are also present and may act as functional elements. One of the AT-rich tandem repeats (AT28) may form interesting structures and is described in detail. The defined features show only a loose resemblance to the structures of known centromeres, highlighting the possibility that, rather than a conserved primary sequence, it is the overall composition and distribution patterns of various unknown functional elements, or any 'ordinary' DNA under appropriate epigenetic influences, that determine centromere formation and function. This is the first detailed analysis of a ***neocentromere*** DNA and provides a basis for comparison against future sequences.

L6 ANSWER 10 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1998:165694 BIOSIS
DN PREV199800165694
TI Direct cloning of human 10q25 ***neocentromere*** DNA using transformation-associated recombination (TAR) in yeast.
AU Cancilla, Michael R.; Tainton, Kellie M.; Barry, Alyssa E.; Larionov, Vladimir; Kouprina, Natalya; Resnick, Michael A.; Du Sart, Desiree; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst. Res. Birth Defects, Royal Children's Hosp., Flemington Road, Parkville 3052, Australia
SO Genomics, (Feb. 1, 1998) Vol. 47, No. 3, pp. 399-404. print.
CODEN: GNMCEP. ISSN: 0888-7543.
DT Article
LA English
ED Entered STN: 6 Apr 1998
Last Updated on STN: 6 Apr 1998
AB The transformation-associated recombination (TAR) procedure allows rapid, site-directed cloning of specific human chromosomal regions as yeast artificial chromosomes (YACs). The procedure requires knowledge of only a single, relatively small genomic sequence that resides adjacent to the chromosomal region of interest. We applied this approach to the cloning of the ***neocentromere*** DNA of a marker chromosome that we have previously shown to have originated through the activation of a latent centromere at human chromosome 10q25. Using a unique 1.4-kb DNA fragment
as a "hook" in TAR experiments, we achieved single-step isolation of the critical ***neocentromere*** DNA region as two stable, 110- and 80-kb circular YACs. For obtaining large quantities of highly purified DNA, these YACs were retrofitted with the yeast-bacteria-mammalian-cells shuttle vector BRV1, electroporated into Escherichia coli DH10B, and isolated as bacterial artificial chromosomes (BACs). Extensive characterization of these YACs and BACs by PCR and restriction analyses revealed that they are identical to the corresponding regions of the normal ***chromosome*** ***10*** and provided further support for the formation of the ***neocentromere*** within the marker chromosome through epigenetic activation.

L6 ANSWER 11 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1998:30117 BIOSIS
DN PREV199800030117
TI ***Neocentromere*** -mediated chromosome movement in maize.
AU Yu, Hong-Guo; Hiatt, Evelyn N.; Chan, Annette; Sweeney, Mary; Dawe, R. Kelly [Reprint author]
CS Dep. Bot., Miller Plant Sci. Build., Univ. Georgia, Athens, GA 30602, USA
SO Journal of Cell Biology, (Nov. 17, 1997) Vol. 139, No. 4, pp. 831-840. print.
CODEN: JCLBA3. ISSN: 0021-9525.
DT Article
LA English
ED Entered STN: 14 Jan 1998
Last Updated on STN: 14 Jan 1998
AB ***Neocentromere*** activity is a classic example of nonkinetochore chromosome movement. In maize, neocentromeres are induced by a gene or genes on Abnormal ***chromosome*** ***10*** (Ab10) which causes heterochromatic knobs to move poleward at meiotic anaphase. Here we describe experiments that test how ***neocentromere*** activity affects the function of linked centromere/kinetochores (kinetochores) and whether neocentromeres and kinetochores are mobilized on the spindle by the same mechanism. Using a newly developed system for observing meiotic chromosome congression and segregation in living maize cells, we show that neocentromeres are active from prometaphase through anaphase. During mid-anaphase, normal chromosomes move on the spindle at an average rate of 0.79 mum/min. The presence of Ab10 does not affect the rate of normal chromosome movement but propels neocentromeres poleward at rates as high as 1.4 mum/min. Kinetochore-mediated chromosome movement is only marginally affected by the activity of a linked ***neocentromere*** . Combined in situ hybridization/immunocytochemistry is used to demonstrate that unlike kinetochores, neocentromeres associate laterally with microtubules and that ***neocentromere*** movement is correlated with knob size. These data suggest that microtubule depolymerization is not required for ***neocentromere*** motility. We argue that neocentromeres are mobilized on microtubules by the activity of minus end-directed motor proteins that interact either directly or indirectly with knob DNA sequences.

L6 ANSWER 12 OF 17 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1987:61617 BIOSIS
DN PREV198783029943; BA83:29943
TI PREFERENTIAL SEGREGATION INVOLVING A KNOBLESS CHROMOSOME IN MAIZE.
AU SARAIVA L S [Reprint author]
CS DEP BIOLOGIA GERAL UFV 36570 VICOSA, MG
SO Revista Ceres, (1986) Vol. 33, No. 186, pp. 165-172.

CODEN: RCERA2. ISSN: 0034-737X.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 24 Jan 1987
Last Updated on STN: 24 Jan 1987
AB A translocated chromosome (9B) arose in which all of the distal heterochromatin of the B chromosome was attached to the short arm of chromosome 9 in maize. Test for preferential segregation of 9B during megasporogenesis in plants heterozygous for a normal knobless chromosome 9 (k9) and the translocated 9B and carrying the abnormal ***chromosome*** ***10*** (K10) gave unexpected results. The k9 was favored over the 9B chromosome, the translocation being recovered in only about 38% of the ovules. The preferential segregation of the knobless chromosome was not associated with ***neocentromere*** formation. Thus, the distal heterochromatin of the B chromosome following transposition does not acquire the property of the heterochromatin knobs in associating with K10 to be recovered preferentially, but remains passive. The mechanism of preferential segregation of the knobless intact chromosome 9 remains to be elucidated.

L6 ANSWER 13 OF 17 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN
AN 2001045989 EMBASE
TI Prenatal molecular cytogenetic diagnosis of partial tetrasomy 10p due to ***neocentromere*** formation in an inversion duplication analphoid marker chromosome.
AU Levy B.; Papenhausen P.R.; Tepperberg J.H.; Dunn T.M.; Fallet S.; Magid M.S.; Kardon N.B.; Hirschhorn K.; Warburton P.E.
CS Dr. B. Levy, Department of Human Genetics, Box 1497, Mount Sinai School of Medicine, One Gustave L. Levy Place, New York, NY 10029, United States. brynn.levy@mssm.edu
SO Cytogenetics and Cell Genetics, (2000) 91/1-4 (165-170).
Refs: 41
ISSN: 0301-0171 CODEN: CGCGBR
CY Switzerland
DT Journal; Article
FS 010 Obstetrics and Gynecology
022 Human Genetics
LA English
SL English
AB Neocentromeres are fully functional centromeres found on rearranged or marker chromosomes that have separated from endogenous centromeres. Neocentromeres often result in partial tri- or tetrasomy because their formation confers mitotic stability to acentric chromosome fragments that would normally be lost. We describe the prenatal identification and characterization of a de novo supernumerary marker chromosome (SMC) containing a ***neocentromere*** in a 20-wk fetus by the combined use of comparative genomic hybridization (CGH) and fluorescence in situ hybridization (FISH). GTG-banding of fetal metaphases revealed a 47,XY,+mar karyotype in 100% of cultured amniocytes; parental karyotypes were both normal. Although sequential tricolor FISH using chromosome-specific painting probes identified a ***chromosome*** ***10*** origin of the marker, a complete panel of chromosome-specific centromeric satellite DNA probes failed to hybridize to any portion of the marker. The presence of a ***neocentromere*** on the marker chromosome was confirmed by the absence of hybridization of an all-human-centromere alpha-satellite DNA probe, which hybridizes to all normal centromeres, and the presence of centromere protein (CENP)-C, which is associated specifically with active kinetochores. Based on CGH analysis and FISH with a chromosome 10p subtelomeric probe, the marker was found to be an inversion duplication of the distal portion of chromosome 10p. Thus, the proband's karyotype was 47,XY,+inv dup(10)(pter fwdarw p14 .apprx. 15::p14 .apprx. 15 fwdarw neo fwdarw pter),which is the first report of partial tetrasomy 10p resulting from an analphoid marker chromosome with a ***neocentromere*** . This study illustrates the use of several molecular strategies in distinguishing centric alphoid markers from neocentric analphoid markers. Copyright .COPYRGT. 2001 S. Karger AG, Basel.

L6 ANSWER 14 OF 17 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN
AN 2000236117 EMBASE
TI Acquisition and metastability of centromere identity and function: Sequence analysis of a human ***neocentromere*** .
AU Maggert K.A.; Karpen G.H.
CS G.H. Karpen, MBVL, Salk Institute, 10010 North Torrey Pines Road, La Jolla, CA 92037, United States. karpen@salk.edu
SO Genome Research, (2000) 10/6 (725-728).
Refs: 34
ISSN: 1088-9051 CODEN: GEREFS
CY United States
DT Journal; General Review
FS 022 Human Genetics
LA English

L6 ANSWER 15 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2004:710413 CAPLUS
TI Effects of Scaffold/Matrix Alteration on Centromeric Function and Gene Expression
AU Sumer, Huseyin; Saffery, Richard; Wong, Nicholas; Craig, Jeffrey M.; Choo, K. H. Andy
CS Murdoch Childrens Research Institute, Department of Pediatrics, Royal Children's Hospital, Flemington Road, Melbourne, 3052, Australia
SO Journal of Biological Chemistry (2004), 279(36), 37631-37639
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB We have previously described a 3.5-Mb domain of enhance scaffold/matrix attachment region (S/MAR) at a human ***neocentromere*** , and normal expression of underlying genes within this region. We also reported that partial inhibition of histone deacetylation using 33 nMtrichostatin A (TSA) resulted in a shift in the position of the CENP-A-binding domain within the ***neocentromere*** , with no noticeable effects on mitotic segregation function. In this study, 33 nM TSA caused a redn. in the size of the enhanced S/MAR domain of one-half to 1.7 Mb. Treatment with a DNA-intercalating drug distamycin A (DST) at 75 .mu.g/mL resulted in a size redn. of the enhanced S/MAR domain at the ***neocentromere*** of two-thirds to 1.2 Mb, and that of the CENP-A-binding domain of 40%, from 330 to 196 kb, with no significant shift in the position of the latter domain. Other DST effects include mitotic chromosomal missegregation, redn. in the levels of Topo II.alpha., CENP-A, CENP-C, and HP1.alpha., and an increase in mitotic checkpoint protein BubR1. TSA or DST treatment similarly resulted in a significant redn., by .apprx.20 and 50%, resp., in the size of the enhanced S/MAR domain at the .alpha.-satellite DNA of a native ***chromosome*** ***10*** centromere. Transcriptional competence within the ***neocentromere*** is overall not noticeably altered by either TSA or DST treatment, as is evident from the absence of any significant increase or decrease in the expression levels of 47 underlying genes tested. These results suggest that a substantial contraction of the S/MAR domain may not be deleterious to centromere function, that disruption of the S/MAR domain directly affects the binding properties of a host of scaffold/matrix and centromeric/pericentric proteins, and that the overall competence and regulation of transcription at the neocentromeric chromatin is similar to those found at the corresponding normal genomic sites.

L6 ANSWER 16 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:176717 CAPLUS
DN 130:292305
TI Sequence analysis of an 80 kb human ***neocentromere*** . [Erratum to document cited in CA130:262978]
AU Barry, Alyssa E.; Howman, Emily V.; Cancilla, Michael R.; Saffery, Richard; Choo, K. H. Andy
CS The Murdoch Institute, Royal Children's Hospital, Parkville, Australia
SO Human Molecular Genetics (1999), 8(3), 551
CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB The DDBJ/EMBL/GenBank accession no. for this paper was printed incorrectly; it should be AF042484.

L6 ANSWER 17 OF 17 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:761972 CAPLUS
DN 129:340539
TI Neocentromeric DNA sequence from human chromosome 10q25 with uses as artificial chromosome vectors
IN Choo, Kong-Hong Andy; Du Sart, Desiree; Cancilla, Michael Robert
PA Amrad Operations Pty. Ltd., Australia
SO PCT Int. Appl., 540 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9851790	A1	19981119	WO 1998-AU352	19980513
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9873258	A1	19981208	AU 1998-73258	19980513
AU 731572	B2	20010405		
EP 996719	A1	20000503	EP 1998-920396	19980513
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 6265211	B1	20010724	US 1998-78294	19980513
US 2003096398	A1	20030522	US 2000-728552	20001202
PRAI AU 1997-6784	A	19970513		
AU 1997-8791	A	19970826		
US 1998-78294	A1	19980513		
WO 1998-AU352	W	19980513		

AB The present invention is directed generally to an isolated nucleic acid mol. encompassing a ***neocentromere*** or a functional deriv. thereof or a latent, synthetic or hybrid form thereof and its use inter alia in developing a range of eukaryotic artificial chromosomes including mammalian (e.g. human) and non-mammalian artificial chromosomes. An unusual human marker chromosome, mardel 10, is identified which is 100% stable in mitotic division both in the original patient and in established

fibroblast and transformed lymphoblast cultures. A region of the mardel (10) chromosome was cloned together with the corresponding region from a normal human subject. The nucleic acid mols. cloned contain no substantial .alpha.-satellite repeats yet are mitotically stable. The nucleic acid mols. encompass, therefore, a new form of centromere referred to as a ***neocentromere*** . The identification and cloning of a eukaryotic ***neocentromere*** without substantial .alpha.-satellite DNA repeat sequences provides a means of generating a range of eukaryotic artificial chromosomes such as mammalian including human artificial chromosomes with uses in genetic therapy, transgenic plant and animal prodn. and recombinant protein prodn. A range of diagnostic reagents is now also obtainable using the cloned ***neocentromere*** .
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> s l1 and py<=1997
2 FILES SEARCHED...
L7 11 L1 AND PY<=1997

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 6 DUP REM L7 (5 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 1
AN 1998:93564 BIOSIS
DN PREV199800093564
TI Centromere DNA dynamics: Latent centromeres and ***neocentromere*** formation.
AU Choo, K. H. Andy [Reprint author]
CS Murdoch Inst. Res. Birth Defects, Royal Children's Hosp., Flemington Road, Parkville 3052, Australia
SO American Journal of Human Genetics, (Dec., 1997) Vol. 61, No. 6, pp. 1225-1233. print.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 25 Feb 1998
Last Updated on STN: 25 Feb 1998

L8 ANSWER 2 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 2
AN 1998:30117 BIOSIS
DN PREV199800030117
TI ***Neocentromere*** -mediated chromosome movement in maize.
AU Yu, Hong-Guo; Hiatt, Evelyn N.; Chan, Annette; Sweeney, Mary; Dawe, R. Kelly [Reprint author]
CS Dep. Bot., Miller Plant Sci. Build., Univ. Georgia, Athens, GA 30602, USA
SO Journal of Cell Biology, (Nov. 17, 1997) Vol. 139, No. 4, pp. 831-840. print.
CODEN: JCLBA3. ISSN: 0021-9525.
DT Article
LA English
ED Entered STN: 14 Jan 1998
Last Updated on STN: 14 Jan 1998
AB ***Neocentromere*** activity is a classic example of nonkinetochore chromosome movement. In maize, neocentromeres are induced by a gene or genes on Abnormal chromosome 10 (Ab10) which causes heterochromatic knobs
to move poleward at meiotic anaphase. Here we describe experiments that test how ***neocentromere*** activity affects the function of linked centromere/kinetochores (kinetochores) and whether neocentromeres and kinetochores are mobilized on the spindle by the same mechanism. Using a newly developed system for observing meiotic chromosome congression and segregation in living maize cells, we show that neocentromeres are active from prometaphase through anaphase. During mid-anaphase, normal chromosomes move on the spindle at an average rate of 0.79 mum/min. The presence of Ab10 does not affect the rate of normal chromosome movement but propels neocentromeres poleward at rates as high as 1.4 mum/min. Kinetochore-mediated chromosome movement is only marginally affected by the activity of a linked ***neocentromere*** . Combined in situ hybridization/immunocytochemistry is used to demonstrate that unlike kinetochores, neocentromeres associate laterally with microtubules and that ***neocentromere*** movement is correlated with knob size. These data suggest that microtubule depolymerization is not required for ***neocentromere*** motility. We argue that neocentromeres are mobilized on microtubules by the activity of minus end-directed motor proteins that interact either directly or indirectly with knob DNA sequences.

L8 ANSWER 3 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1998:110733 BIOSIS
DN PREV199800110733
TI Inv dup(13)(qterq21.1) with ***neocentromere*** in 13q32: Precise definition of duplication and centromere location using cenp antibodies and FISH.
AU Warburton, D. [Reprint author]; Perricone, L.; Say, B.; Carpenter, N.; Yu, C.-Y. [Reprint author]; Warburton, P. E.
CS Columbia Univ., New York, NY, USA
SO American Journal of Human Genetics, (Oct., 1997) Vol. 61, No. 4 SUPPL., pp. A142. print.
Meeting Info.: 47th Annual Meeting of the American Society of Human Genetics. Baltimore, Maryland, USA. October 28-November 1, 1997.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Mar 1998
Last Updated on STN: 3 Mar 1998

L8 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 3
AN 1993:522989 BIOSIS
DN PREV199396136396
TI Molecular characterization of a maize B chromosome centric sequence.
AU Alfenito, Mark R. [Reprint author]; Birchler, James A.
CS Dep. Biol. Sci., Stanford Univ., Stanford, Calif. 94305-5020, USA
SO Genetics, (1993) Vol. 135, No. 2, pp. 589-597.
CODEN: GENTAE. ISSN: 0016-6731.
DT Article
LA English
OS EMBL-L14275; Genbank-L14275
ED Entered STN: 19 Nov 1993
Last Updated on STN: 19 Nov 1993
AB Supernumerary chromosomes are widespread in the plant kingdom but little is known of their molecular nature or mechanism of origin. We report here the initial cloning of sequences from the maize B chromosome. Our analysis suggests that many sequences are highly repetitive and shared with the normal A chromosomes. However, all clones selected for B-specificity contain at least one copy of a particular repeat. Cytological mapping using B chromosome derivatives and in situ hybridization show that the B specific repeats are derived from the centric region of the chromosome. Sequence analysis of this repeat shows homology to motifs mapped to various plant and animal centromeres and to the maize ***neocentromere*** . A precise localization of these sequences among breakpoints within the B centromere and an homology to a facultative centromere, suggest a role for this sequence is centromere function.

L8 ANSWER 5 OF 6 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1987:61617 BIOSIS
DN PREV198783029943; BA83:29943
TI PREFERENTIAL SEGREGATION INVOLVING A KNOBLESS CHROMOSOME IN MAIZE.
AU SARAIVA L S [Reprint author]
CS DEP BIOLOGIA GERAL UFV 36570 VICOSA, MG
SO Revista Ceres, (1986) Vol. 33, No. 186, pp. 165-172.
CODEN: RCERA2. ISSN: 0034-737X.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 24 Jan 1987
Last Updated on STN: 24 Jan 1987
AB A translocated chromosome (9B) arose in which all of the distal heterochromatin of the B chromosome was attached to the short arm of chromosome 9 in maize. Test for preferential segregation of 9B during megasporogenesis in plants heterozygous for a normal knobless chromosome 9 (k9) and the translocated 9B and carrying the abnormal chromosome 10 (K10) gave unexpected results. The k9 was favored over the 9B chromosome, the translocation being recovered in only about 38% of the ovules. The preferential segregation of the knobless chromosome was not associated with ***neocentromere*** formation. Thus, the distal heterochromatin of the B chromosome following transposition does not acquire the property of the heterochromatin knobs in associating with K10 to be recovered preferentially, but remains passive. The mechanism of preferential segregation of the knobless intact chromosome 9 remains to be elucidated.

L8 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1974:116674 CAPLUS
DN 80:116674
TI Chromosomal damage and abnormal seedling development in barley induced by
chemical treatment with TIBA [2,3,5-triiodobenzoic acid], maleic hydrazide, and formamide
AU Price, Mazo; Schank, S. C.
CS Agron. Dep., Univ. Florida, Gainesville, FL, USA
SO Proceedings - Soil and Crop Science Society of Florida (***1973***), Volume Date 1972, 32, 41-6
CODEN: SCSFAD; ISSN: 0096-4522
DT Journal
LA English
AB Chromosomal breakage and abnormal seedling development were induced in barley by soaking of barley seeds for 12 hr in formamide [75-12-7] (0.5, 0.1, or 0.05M), maleic hydrazide [123-33-1] (0.1 and 0.001M), or

2,3,5-triiodobenzoic acid (I) [88-82-4] (0.001 or 0.0001M). All 3 compds. decreased germination, root length, and seedling height, produced chromosome breakage in root tip cells and in the pollen mother cells, and induced pollen sterility. Chromosome breakages induced by formamide and maleic hydrazide were localized in heterochromatic segments close to or at the centromere, causing ***neocentromere*** formation. I-induced breakages were not in specific centromeric regions and frequently yielded translocations.

=> s centromere
L9 18451 CENTROMERE

=> s l9 and human artificial chromosome
L10 49 L9 AND HUMAN ARTIFICIAL CHROMOSOME

=> s l9 and mammal? artificial chromosome
L11 49 L9 AND MAMMAL? ARTIFICIAL CHROMOSOME

=> s l10 or l11
L12 95 L10 OR L11

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13 57 DUP REM L12 (38 DUPLICATES REMOVED)

=> s l13 and PY<=1997
2 FILES SEARCHED...
L14 12 L13 AND PY<=1997

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 12 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1997:438961 BIOSIS
DN PREV199799738164
TI Human centromeric DNAs.
AU Lee, C.; Wevrick, R.; Fisher, R. B.; Ferguson-Smith, M. A. [Reprint author]; Lin, C. C.
CS Dep. Pathol., Univ. Cambridge, Tennis Court Road, Cambridge CB2 1QP, UK
SO Human Genetics, (1997) Vol. 100, No. 3-4, pp. 291-304.
CODEN: HUGEDQ. ISSN: 0340-6717.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997
AB Human centromeres have been extensively studied over the past two decades.
Consequently, more is known of ***centromere*** structure and organization in humans than in any other higher eukaryote species. Recent advances in the construction of a human (or ***mammalian***) ***artificial*** ***chromosome*** have fostered increased interest in determining the structure and function of fully functional human centromeres. Here, we present an overview of currently identified human centromeric repetitive DNA families: their discoveries, molecular characterization, and organization with respect to other centromeric repetitive DNA families. A brief examination of some functional based studies is also included.

L14 ANSWER 2 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1997:221345 BIOSIS
DN PREV199799513061
TI Centromeres, CENP-B and Tigger too.
AU Kipling, David [Reprint author]; Warburton, Peter E.
CS MRC Hum. Genet. Unit, Western Gen. Hosp., Crewe Rd., Edinburgh EH4 2XU, UK
SO Trends in Genetics, (1997) Vol. 13, No. 4, pp. 141-145.
CODEN: TRGEE2. ISSN: 0168-9525.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997

L14 ANSWER 3 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1997:110025 BIOSIS
DN PREV199799409228
TI Mammalian artificial chromosomes: A review.
AU Sgaramella, Vittorio; Eridani, Sandro
CS ITBA, Natl. Res. Council, Via Ampere 56, Milano, Italy
SO Cytotechnology, (1996) Vol. 21, No. 3, pp. 253-261.
ISSN: 0920-9069.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 10 Mar 1997
Last Updated on STN: 10 Mar 1997
AB A ***mammalian*** ***artificial*** ***chromosome*** (MAC) may be assembled through the juxtapposition of three kinds of DNA elements: a ***centromere*** , several DNA replication origins, and two telomeric repeats. The resulting structure should be able to carry and express one or more selected genes (transgenes), introduced for specific purposes. The minimal length is unknown, but may be of several Mb. Of its basic elements, the telomeres may present lesser problems, in view of their simple composition and organization. Centromeres could be an issue, given their many unknowns. Mammalian DNA replication origins are at present poorly characterized, but it is expected that at least one may be contained within the MAC components, especially the transgene. Their overall assembly may require a combination of in vivo and in vitro approaches. A promising strategy aims at constructing two telomeric arms of a MAC, one of which may include the transgene. The two novel arms could acquire a functional ***centromere*** through recombination with the two arms of a resident chromosome. Alternatively, if the two telomeric constructs are also endowed with properly placed and oriented centromeric sequences, a ***centromere*** may be rescued in vivo by homologous recombination with the external parts of the ***centromere*** of the resident chromosome. Positive selection for the artificial arms and counterselection against the resident arms should facilitate the assembly process. The assembly of such construct would not change the ploidy number of the host cell. After loading of a transgene, however, the resulting MAC may be isolated and transferred into an expression cell, where it may represent a novel chromosomal element. In this case untoward effects to the host cell may derive from an ensuing dosage effect for the transgene(s) rather than from the presence of a MAC per se. A MAC may contribute to a deeper understanding of the structural requirements for chromosomal function and evolution as well as the mechanism of chromatin formation. It should also help in the development of second generation vectors for transfer of Mb-long DNA sequences, as required for properly regulated mammalian gene function as well as, possibly, for therapy.

L14 ANSWER 4 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:484437 BIOSIS
DN PREV199699199693
TI Analysis of extrachromosomal structures containing human centromeric alphoid satellite DNA sequences in mouse cells.
AU Taylor, Stephen S. [Reprint author]; Larin, Zoia; Tyler-Smith, Chris
CS Dep. Cell Biol., Harvard Med. Sch., 240 Longwood Ave., Boston, MA 02115, USA
SO Chromosoma (Berlin), (1996) Vol. 105, No. 2, pp. 70-81.
CODEN: CHROAU. ISSN: 0009-5915.
DT Article
LA English
ED Entered STN: 24 Oct 1996
Last Updated on STN: 24 Oct 1996
AB Yeast artificial chromosomes (YACs) spanning the centromeric region of the human Y chromosome were introduced into mouse LA-9 cells by spheroplast fusion in order to determine whether they would form mammalian artificial chromosomes. In about 50% of the cell lines generated, the YAC DNA was associated with circular extrachromosomal structures. These episomes were only present in a proportion of the cells, usually at high copy number, and were lost rapidly in the absence of selection. These observations suggest that, despite the presence of centromeric sequences, the structures were not segregating efficiently and thus were not forming artificial chromosomes. However, extrachromosomal structures containing alphoid DNA appeared cytogenetically smaller than those lacking it, as long as yeast DNA was also absent. This suggests that alphoid DNA can generate the condensed chromatin structure at the ***centromere*** .

L14 ANSWER 5 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:35615 BIOSIS
DN PREV199698607750
TI Generation of a human X-derived minichromosome using telomere-associated chromosome fragmentation.
AU Farr, Christine J. [Reprint author]; Bayne, Rosemary A. L.; Kipling, David; Mills, Walter; Critcher, Ricky; Cooke, Howard J.
CS Dep. Genet., Univ. Cambridge, Downing St., Cambridge CB2 3EH, UK
SO EMBO (European Molecular Biology Organization) Journal, (1995) Vol. 14, No. 21, pp. 5444-5454.
CODEN: EMJODG. ISSN: 0261-4189.
DT Article
LA English
ED Entered STN: 26 Jan 1996
Last Updated on STN: 26 Jan 1996
AB A linear ***mammalian*** ***artificial*** ***chromosome*** vector will require at least three functional elements: a ***centromere*** , two telomeres and replication origins. One route to generate such a vector is by the fragmentation of an existing chromosome. We have previously described the use of cloned telomeric DNA to generate and stably rescue truncated derivatives of a human X chromosome in a somatic cell hybrid. Further rounds of telomere-associated chromosome fragmentation have now been used to engineer a human X-derived minichromosome. This minichromosome is estimated to be lt 10 Mb in size. In situ hybridization and molecular analysis reveal that the minichromosome has a linear structure, with two introduced telomere constructs flanking a 2.5 Mb a-satellite array. The highly truncated chromosome also retains some chromosome-specific DNA, originating from

Xp11.21. There is no significant change in the mitotic stability of the minichromosome as compared with the X chromosome from which it was derived.

L14 ANSWER 6 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1994:498814 BIOSIS
DN PREV199497511814
TI Addition of functional human telomeres to YACs.
AU Taylor, Stephen S. [Reprint author]; Larin, Zoia; Smith, Chris Tyler
CS CRC chromosome Molecular Biol. Group, Dep. Biochem., Univ. Oxford, South Parks Road, Oxford OX1 3QU, UK
SO Human Molecular Genetics, (1994) Vol. 3, No. 8, pp. 1383-1386. ISSN: 0964-6906.
DT Article
LA English
ED Entered STN: 28 Nov 1994
Last Updated on STN: 28 Nov 1994
AB Linear mammalian artificial chromosomes (MACs) will require functional telomeres, a ***centromere*** and the ability to replicate autonomously. We are investigating the possibility of developing MACs from yeast artificial chromosomes (YACs). Retrofitting vectors have been constructed to replace YAC telomeres with cloned human telomeric DNA. A modified YAC was introduced into mammalian cells by spheroplast fusion and the frequency with which the retrofitted human telomeric DNA seeded the formation of a new telomere was determined by Bal31 digestion and cytogenetic analysis. The telomere adjacent to the selectable marker gene was functional in 5/46 clones (11%) while the telomere 200 kb away at the other end of the YAC was functional in 1/46 clones (2%). These results indicate that despite the in vivo modification of the end of the telomere by the addition of yeast sequences, human telomeres will function at a high enough frequency to allow the construction of MACs by this route.

L14 ANSWER 7 OF 12 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1994:482565 BIOSIS
DN PREV199497495565
TI Mammalian artificial chromosomes: A new tool for gene therapy.
AU Huxley, Clare
CS Dep. Biochem. Mol. Genetics, St. Mary's Hosp. Med. Sch., Norflok Place, London W2 1PG, UK
SO Gene Therapy, (1994) Vol. 1, No. 1, pp. 7-12.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 9 Nov 1994
Last Updated on STN: 9 Nov 1994
AB Effective therapy by in vivo delivery of DNA requires efficient delivery, long-term maintenance of the DNA that is delivered and physiological levels of expression of the therapeutic gene. Full levels of physiologically controlled expression can be obtained after transfer of intact genes on fragments of DNA hundreds of kilobases in size, as has been demonstrated by the transfer of yeast artificial chromosomes into transgenic mice. Long-term maintenance of input DNA could be achieved if the DNA carried replication origins, a ***centromere*** and telomeres to allow maintenance and segregation in mammalian cells, and there has been recent progress towards cloning these elements. These features could be combined as a ***mammalian*** ***artificial*** ***chromosome*** which would confer full levels of controlled expression as well as being maintained in any cell into which it was introduced. Methods which would allow delivery of such large fragments of DNA include liposomes and receptor-mediated uptake, both of which have been shown to work in vivo, making such large constructs potentially applicable for use in gene therapy.

L14 ANSWER 8 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:718036 CAPLUS
DN 128:19355
TI methods for prepg. mammalian artificial chromosomes (MACs)
IN Hadlaczky, Gyula; Szalay, Aladar A.
PA Hadlaczky, Gyula, Hung.; Szalay, Aladar A.; American Gene Therapy, Inc.; Biological Research Center of the Hungarian Academy of Sciences; Loma Linda University
SO PCT Int. Appl., 248 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9740183	A2	19971030	WO 1997-US5911	19970410 <--
WO 9740183	A3	19980205		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6077697	A	20000620	US 1996-682080	19960715
US 6025155	A	20000215	US 1996-695191	19960807
AU 9724512	A1	19971112	AU 1997-24512	19970410 <--
EP 929689	A2	19990721	EP 1997-920284	19970410
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9708855	A	20000104	BR 1997-8855	19970410
NZ 331815	A	20000428	NZ 1997-331815	19970410
JP 2000508177	T2	20000704	JP 1997-538116	19970410
AU 773728	B2	20040603	AU 2001-38957	20010430
US 2004143861	A1	20040722	US 2004-782129	20040218
PRAI US 1996-629822	A	19960410		
US 1996-682080	A	19960715		
US 1996-695191	A	19960807		
US 1996-682191	A	19960715		
AU 1997-24512	A3	19970410		
WO 1997-US5911	W	19970410		
US 1998-96648	A1	19980612		

AB Methods for prepg. cell lines that contain artificial chromosomes, methods for prepn. of artificial chromosomes, methods for purifn. of artificial chromosomes, methods for targeted insertion of heterologous DNA into artificial chromosomes, and methods for delivery of the chromosomes to selected cells and tissues are provided. Also provided are cell lines for use in the methods, and cell lines and chromosomes produced by the methods. In particular, satellite artificial chromosomes [SATACs] that, except for inserted heterologous DNA, are substantially composed of heterochromatin, are provided. Methods for use of the artificial chromosomes, including for gene therapy, prodn. of gene products and prodn. of transgenic plants and animals are also provided.

L14 ANSWER 9 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:663610 CAPLUS
DN 127:355670
TI Mammalian artificial chromosomes - vectors for somatic gene therapy
AU Ascenzioni, F.; Donini, P.; Lipps, H. J.
CS Instituto Pasteur, Fondazione Cenci Bolognetti, c/o Dipartimento di Biologia cellulare e dello Sviluppo, University of Rome, Rome, Italy
SO Cancer Letters (Shannon, Ireland) (***1997***), 118(2), 135-142
CODEN: CALEDQ; ISSN: 0304-3835
PB Elsevier
DT Journal; General Review
LA English
AB A review with 63 refs. Mammalian artificial chromosomes might prove to be useful vectors for somatic gene therapy. The functional elements of such an artificial chromosome are telomeres, a ***centromere*** and a replication origin. Recent progress in the characterization of these functional elements of the eukaryotic chromosome will be described. Attempts to construct artificial chromosomes for mammalian cells and their use for somatic gene therapy are discussed.

L14 ANSWER 10 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:414064 CAPLUS
DN 127:30119
TI Mammalian artificial chromosomes, method for their preparation, and their use for expression of genes in mammalian cells
IN Scheffler, Immo E.
PA Regents of the University of California, USA
SO PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9716533	A1	19970509	WO 1996-US17476	19961029 <--
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
PRAI US 1995-550717		19951031		

AB The present invention provides a ***mammalian*** ***artificial*** ***chromosome*** (MAC), comprising a ***centromere*** and a unique cloning site, said MAC contg. less than 0.1% of the DNA present in a normal haploid genome or the mammalian cell from which the ***centromere*** was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of prepg. a MAC. In addn., the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC contg. the selectable marker into the cell. The invention also provides a cell contg. a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker. Human X hamster hydrid cells XJM12.1.3 contg. human chromosome 1 minichromosome were irradiated to prep. XEW8.2.3 cells contg. a minichromosome contg. 1-2 million base pairs of DNA from the short arm of chromosome 1. This minichromosome was found to contain the gene for subunit CII-3 of complex II of the mitochondrial electron transport chain. The cDNA for this gene was cloned and sequenced.

L14 ANSWER 11 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:219195 CAPLUS
DN 126:288624
TI Formation of de novo centromeres and construction of first-generation human artificial microchromosomes
AU Harrington, John J.; Van Bokkelen, Gil; Mays, Robert W.; Gustashhaw, Karen; Willard, Huntington F.

CS Dep. Genetics and Center Human Genetics, Case Western Reserve Univ. Sch.
Med., Cleveland, OH, 44106, USA
SO Nature Genetics (***1997***), 15(4), 345-355
CODEN: NGENEC; ISSN: 1061-4036
PB Nature Publishing Co.
DT Journal
LA English
AB Long synthetic arrays of .alpha. satellite DNA were combined with telomeric DNA and genomic DNA to generate artificial chromosomes in human HT1080 cells. The resulting linear microchromosomes contain exogenous .alpha. satellite DNA, are mitotically and cytogenetically stable in the absence of selection of up to 6 mo in culture, bind ***centromere*** proteins specific for active centromeres, and are estd. to be 6-10 megabases in size, apprx.10-20% the size of endogenous human chromosomes.
Thus, this strategy results in the formation of de novo ***centromere*** activity and the microchromosomes so generated contain all of the sequence elements required for stable mitotic chromosome segregation and maintenance. This first-generation system for the construction of human artificial chromosomes should be suitable for dissecting the sequence requirements of human centromeres, as well as developing constructs useful for therapeutic applications.

L14 ANSWER 12 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:76579 CAPLUS
DN 124:108957
TI Functional ***centromere*** elements derived from mammalian chromosomes for use in the construction of ***mammalian*** ***artificial*** ***chromosome*** vectors
IN Brown, William
PA Cancer Research Campaign Technology Ltd., UK
SO PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9532297	A1	19951130	WO 1995-GB1195	19950525 <--
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9525343	A1	19951218	AU 1995-25343	19950525 <--
ZA 9504300	A	19960124	ZA 1995-4300	19950525 <--
PRAI GB 1994-10446		19940525		
WO 1995-GB1195		19950525		

AB The isolation of functional elements of mammalian centromeres for use in the construction of mammalian artificial chromosomes using telomere-directed chromosome fragmentation techniques is described for use in, for instance for application in gene therapy and animal gene transfer. These vectors are capable of replication and segregation during cell cycle, and are of a size that can be resolved using gel electrophoresis. Suitable fragments are derived from the human Y chromosome. The generation of truncated human Y-chromosomes that are stable in mitosis is demonstrated.

=> s latent (3a) centromere
L15 32 LATENT (3A) CENTROMERE

=> dup rem l15
PROCESSING COMPLETED FOR L15
L16 16 DUP REM L15 (16 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 16 ANSWERS - CONTINUE? Y/(N):y

L16 ANSWER 1 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 1
AN 2002:173993 BIOSIS
DN PREV200200173993
TI In search of a 9q13 ***latent*** ***centromere*** in 9qh polymorphic inversions.
AU Gutierrez-Angulo, M.; Vasquez, A. I.; Ramos, A. L.; Dominguez, M. G.; Gonzalez-Garcia, J. R.; Rivera, H. [Reprint author]
CS Centro de Investigacion Biomedica de Occidente, IMSS, Guadalajara, Jal., Mexico
hrivera@udgserv.cencar.udg.mx
SO Genetic Counseling, (2001) Vol. 12, No. 4, pp. 359-362. print.
ISSN: 1015-8146.
DT Article
LA English
ED Entered STN: 5 Mar 2002
Last Updated on STN: 5 Mar 2002
AB The presence of alphoid sequences in 9q13 has prompted the suggestion that such a region could harbor a ***latent*** ***centromere*** which under certain circumstances may appear as a neocentromere. We tested this hypothesis by means of FISH with a centromere 9-specific alphoid probe in lymphocyte metaphases from 13 unrelated individuals with a 9qh polymorphic inversion. Since all inverted chromosomes had the alphoid signal onto the primary constriction, it was not possible to identify any neocentromere. We believe, however, that the number of cases was not enough to conclude that all the polymorphic inversions of chromosome 9 are genuine.

L16 ANSWER 2 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 2
AN 2001:129753 BIOSIS
DN PREV200100129753
TI Boy with bilateral retinoblastoma due to an unusual ring chromosome 13 with activation of a ***latent*** ***centromere*** .
AU Morrissette, Jennifer J. D.; Celle, Livija; Owens, Nancy L.; Shields, Carol L.; Zackai, Elaine H.; Spinner, Nancy B. [Reprint author]
CS Division of Human Genetics and Molecular Biology, Children's Hospital of Philadelphia, 34th Street and Civic Center Boulevard, 1006 Abramson Research Center, Philadelphia, PA, 19104, USA
spinner@mail.med.upenn.edu
SO American Journal of Medical Genetics, (February 15, 2001) Vol. 99, No. 1, pp. 21-28. print.
ISSN: 0148-7299.
DT Article
LA English
ED Entered STN: 14 Mar 2001
Last Updated on STN: 15 Feb 2002
AB We present a patient with bilateral retinoblastoma and developmental delay who has an abnormal male karyotype containing 47 chromosomes, including an acentric derivative chromosome 13. We postulate that the derivative 13 occurred after a break at 13q14, with the proximal portion of the chromosome forming a ring and the distal portion undergoing duplication. Thus, this patient is trisomic for 13q14fwdarwqter. The derivative chromosome with duplicated distal portion (13q14fwdarwqter) lacked the 13 centromere and was negative for chromosome 13 alpha-satellite DNA by low stringency FISH. Nevertheless, this chromosome is stably transmitted in lymphocytes and fibroblasts. A single primary constriction was observed at band 13q21, consistent with activation of a ***latent*** ***centromere*** (neocentromere) at this band. The neocentromere on der(13) was positive for multiple centromeric proteins, suggesting that it acts as the functional centromere. By FISH, the Rb gene was present on the normal 13, the proximally derived ring chromosome, but not on the derivative chromosome. Although there was no evidence for disruption of the Rb gene, this chromosome rearrangement most likely results in abnormal expression of the Rb gene product.

L16 ANSWER 3 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 2000:360775 BIOSIS
DN PREV200000360775
TI Non-alphoid centromeres in 3 different der(x) chromosome populations in a child with Turner syndrome.
AU Dahoun, Sophie [Reprint author]; Jenny, I. [Reprint author]; Vieux, C. [Reprint author]; Monso-Hinard, C. [Reprint author]; Morris, M. A. [Reprint author]; Jaeggi, E.
CS Cantonal Hospital of Geneva, Geneva, Switzerland
SO European Journal of Human Genetics, (June, 2000) Vol. 8, No. Supplement 1, pp. 85. print.
Meeting Info.: European Human Genetics Conference 2000. Amsterdam, Netherlands. May 27-February 30, 2000. European Society of Human Genetics.
ISSN: 1018-4813.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Paper)
LA English
ED Entered STN: 23 Aug 2000
Last Updated on STN: 8 Jan 2002

L16 ANSWER 4 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 3
AN 1999:339890 BIOSIS
DN PREV199900339890
TI Neocentromere at 13q32 in one of two stable markers derived from a 13q21 break.
AU Rivera, H. [Reprint author]; Vasquez, A. I.; Garcia-Cruz, D.; Crolla, J. A.
CS Division de Genetica, Instituto Mexicano del Seguro Social, Guadalajara, Jal., Mexico
SO American Journal of Medical Genetics, (Aug. 6, 1999) Vol. 85, No. 4, pp. 385-388. print.
ISSN: 0148-7299.
DT Article
LA English
ED Entered STN: 24 Aug 1999
Last Updated on STN: 24 Aug 1999
AB A 10-month-old girl with psychomotor retardation, microcephaly, bilateral microphthalmia, and postaxial polydactyly of the feet was karyotyped using banding techniques and (single or dual color) fluorescent in situ hybridization (FISH) with four probes: D13Z1/D21Z1, pancentromeric, pantelomeric, and a mix of 13q subtelomeric and 13/21 alphoid repeats. She was found to have a 47-chromosome karyotype in which a normal 13 was

replaced by two stable markers derived from a breakpoint at 13q21.1, namely a del(13) (q21.1) and an isofragment(13) (qterfwdarwq21.1::q21.1fwdarwqter). The latter had a single C-negative but Cd-positive primary constriction at 13q32 which, however, was not obvious in about 12% of the cells. FISH studies showed that the small 13q- had the 13-centromere and a 13q telomere (as shown for a specific 13q subtelomeric signal) onto the broken end whereas the isofragment lacked alphoid signals but had 13q subtelomeric sequences on both ends. Parental karyotypes were normal. The patient's rearrangement represents the eighth chromosome-13-derived marker with a nonalphoid neocentromere located at 13q. All in all, such neocentromeres have been described in 29 markers derived from chromosomes 2, 3, 8-11, 13-15, 20, and Y, and plausibly result from the epigenetic activation of a ***latent*** ***centromere*** , which may even be a telomere with neocentric activity. The 18q telomere found in the del(13q) was probably captured from the homologous chromosome.

L16 ANSWER 5 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 4
AN 1998:165694 BIOSIS
DN PREV199800165694
TI Direct cloning of human 10q25 neocentromere DNA using transformation-associated recombination (TAR) in yeast.
AU Cancilla, Michael R.; Tainton, Kellie M.; Barry, Alyssa E.; Larionov, Vladimir; Kouprina, Natalya; Resnick, Michael A.; Du Sart, Desiree; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst. Res. Birth Defects, Royal Children's Hosp., Flemington Road, Parkville 3052, Australia
SO Genomics, (Feb. 1, 1998) Vol. 47, No. 3, pp. 399-404. print.
CODEN: GNMCEP. ISSN: 0888-7543.
DT Article
LA English
ED Entered STN: 6 Apr 1998
Last Updated on STN: 6 Apr 1998
AB The transformation-associated recombination (TAR) procedure allows rapid, site-directed cloning of specific human chromosomal regions as yeast artificial chromosomes (YACs). The procedure requires knowledge of only a single, relatively small genomic sequence that resides adjacent to the chromosomal region of interest. We applied this approach to the cloning of the neocentromere DNA of a marker chromosome that we have previously shown to have originated through the activation of a ***latent*** ***centromere*** at human chromosome 10q25. Using a unique 1.4-kb DNA fragment as a "hook" in TAR experiments, we achieved single-step isolation of the critical neocentromere DNA region as two stable, 110- and 80-kb circular YACs. For obtaining large quantities of highly purified DNA, these YACs were retrofitted with the yeast-bacteria-mammalian-cells shuttle vector BRV1, electroporated into Escherichia coli DH10B, and isolated as bacterial artificial chromosomes (BACs). Extensive characterization of these YACs and BACs by PCR and restriction analyses revealed that they are identical to the corresponding regions of the normal chromosome 10 and provided further support for the formation of the neocentromere within the marker chromosome through epigenetic activation.

L16 ANSWER 6 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 5
AN 1998:93564 BIOSIS
DN PREV199800093564
TI ***Centromere*** DNA dynamics: ***Latent*** centromeres and neocentromere formation.
AU Choo, K. H. Andy [Reprint author]
CS Murdoch Inst. Res. Birth Defects, Royal Children's Hosp., Flemington Road, Parkville 3052, Australia
SO American Journal of Human Genetics, (Dec., 1997) Vol. 61, No. 6, pp. 1225-1233. print.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 25 Feb 1998
Last Updated on STN: 25 Feb 1998

L16 ANSWER 7 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 6
AN 1998:93439 BIOSIS
DN PREV199800093439
TI Interstitial deletion 2P accompanied by marker chromosome formation of the deleted segment resulting in a stable acentric marker chromosome.
AU Petit, P.; Fryns, J. P. [Reprint author]
CS Cent. Human Genet., Herestraat 49, B-3000 Leuven, Belgium
SO Genetic Counseling, (1997) Vol. 8, No. 4, pp. 341-343. print.
ISSN: 1015-8146.
DT Article
LA English
ED Entered STN: 25 Feb 1998
Last Updated on STN: 25 Feb 1998
AB We reexamined a moderately mentally retarded patient with mild dysmorphism previously described with de novo 47, XY, del(2)(p11;p21), +acefr. Using fluorescence in situ hybridization (FISH), we now confirm the chromosome 2 nature of the extra marker resulting from interstitial deletion of del(2)(p11;p21) as well the lack alpha satellite DNA pattern. The authors suggest that a reactivation process of a ***latent*** ***centromere*** may explain the origin of this stable extra marker.

L16 ANSWER 8 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 7
AN 1997:295824 BIOSIS
DN PREV199799595027
TI A functional neo-centromere formed through activation of a ***latent*** human ***centromere*** and consisting of non-alpha-satellite DNA.
AU Du Sart, Desiree; Cancilla, Michael R.; Earle, Elizabeth; Mao, Jen-I; Saffery, Richard; Tainton, Kellie M.; Kalitsis, Paul; Martyn, John; Barry, Alyssa E.; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst. Res. Birth Defects, Royal Child. Hosp., Flemington Rd., Parkville 3052, Australia
SO Nature Genetics, (1997) Vol. 16, No. 2, pp. 144-153.
ISSN: 1061-4036.
DT Article
LA English
ED Entered STN: 9 Jul 1997
Last Updated on STN: 9 Jul 1997
AB We recently described a human marker chromosome containing a functional neo-centromere that binds anticentromere antibodies, but is devoid of centromeric alpha-satellite repeats and derived from a hitherto non-centromeric region of chromosome 10q25. Chromosome walking using cloned single-copy DNA from this region enabled us to identify the antibody-binding domain of this centromere. Extensive restriction mapping indicates that this domain has an identical genomic organization to the corresponding normal chromosomal region, suggesting a mechanism for the origin of this centromere through the activation of a ***latent*** ***centromere*** that exists within 10q25.

L16 ANSWER 9 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1994:524843 BIOSIS
DN PREV199497537843
TI A stable acentric marker chromosome derived from distal 8p: Reactivation of a ***latent*** ancient ***centromere*** at 8p23.1?.
AU Ohashi, H. [Reprint author]; Wakui, K. [Reprint author]; Ogawa, K. [Reprint author]; Okano, T.; Niikawa, N.; Fukushima, Y. [Reprint author]
CS Saitama Child. Med. Cent., Iwatsuki, Japan
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A113.
Meeting Info.: 44th Annual Meeting of the American Society of Human Genetics. Montreal, Quebec, Canada. October 18-22, 1994.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Dec 1994
Last Updated on STN: 3 Dec 1994

L16 ANSWER 10 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 8
AN 1993:499629 BIOSIS
DN PREV199396123636
TI A functional marker centromere with no detectable alpha-satellite, satellite III, or CENP-B protein: Activation of a ***latent*** ***centromere*** ?.
AU Voullaire, Lucille E.; Slater, Howard R.; Petrovic, Vida; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst., Royal Children's Hosp., Flemington Road, Parkville, Victoria 3052, Australia
SO American Journal of Human Genetics, (1993) Vol. 52, No. 6, pp. 1153-1163.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
LA English
ED Entered STN: 5 Nov 1993
Last Updated on STN: 5 Nov 1993
AB We report the investigation of an unusual human supernumerary marker chromosome 10 designated "mar del(10)." This marker is present together with two other marker chromosomes in the karyotype of a boy with mild developmental delay. It has a functional centromere at a primary constriction and is mitotically stable. Fluorescence in situ hybridization (FISH) using alpha-satellite and satellite III DNA as probes failed to detect any signal at the primary constriction site. CENP-B protein could not be demonstrated, although the presence of at least some centromeric proteins was confirmed using a CREST antiserum. Consideration of these and other cytogenetic and FISH results supports a mechanism of formation of the mar del(10) chromosome involving the activation of a ***latent*** intercalary ***centromere*** at 10q25.

L16 ANSWER 11 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1993:215274 BIOSIS
DN PREV199344099774
TI Interstitial deletion and ring chromosome derived from 19q: Proximal 19q trisomy phenotype.
AU Quack, B. [Reprint author]; Van Roy, N.; Verschraegen-Spae, M. R.; Klein,

F.
CS Lab. Cytogenetique, F73011 Chambery Cedex, France
SO Annales de Genetique, (1992) Vol. 35, No. 4, pp. 241-244.
CODEN: AGTQAH. ISSN: 0003-3995.
DT Article
LA English
ED Entered STN: 3 May 1993
Last Updated on STN: 3 May 1993

L16 ANSWER 12 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 9
AN 1992:188670 BIOSIS
DN PREV199293099620; BA93:99620
TI INTERSTITIAL DELETION OF CHROMOSOME 9Q WITH COEXISTENCE OF THE DELETED
SEGMENT AS A RING CHROMOSOME.
AU PFEIFFER R A [Reprint author]; TRAUTMANN U; HIRMER-STOLL R
CS INST HUMANGENETIK FRIEDRICH-ALEXANDER, UNIV ERLANGEN-NUERNBURG,
SCHWABACHANLAGE, 10 D W8520 ERLANGEN, GERMANY
SO Annales de Genetique, (1991) Vol. 34, No. 3-4, pp. 247-251.
CODEN: AGTQAH. ISSN: 0003-3995.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 13 Apr 1992
Last Updated on STN: 13 Apr 1992
AB In a mentally retarded female an interstitial deletion of a chromosome 9 and an additional ring chromosome was shown, which by positive hybridisation with a no 9 library was considered to be the excised segment. The functional centromere and C and DA/DAPI positive material as well on the ring chromosome are explained by a break within the centromere close to the constitutive heterochromatin and supports the hypothesis of " ***latent*** " ***centromere*** (s).

L16 ANSWER 13 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 10
AN 1989:159947 BIOSIS
DN PREV198987082048; BA87:82048
TI A DICENTRIC RECOMBINANT 9 DERIVED FROM A PARACENTRIC INVERSION PHENOTYPE
CYTOGENETICS AND MOLECULAR ANALYSIS OF CENTROMERES.
AU WORSHAM M J [Reprint author]; MILLER D A; DEVRIES J M; MITCHELL A R; BABU
V R; SURLI V; WEISS L; VAN DYKE D L
CS MED GENET, HENRY FORD HOSP, 2799 W GRAND BLVD, DETROIT, MICH 48202, USA
SO American Journal of Human Genetics, (1989) Vol. 44, No. 1, pp. 115-123.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 25 Mar 1989
Last Updated on STN: 25 Mar 1989
AB A 4-year-old girl with multiple malformations and severe developmental delay has been shown to have a karyotype of 46,XX,-9,+rec(9),dup p,inv(9)(q22.1q34.3)mat, with duplication 9pter-q22.1 and deficiency 9q34.3-qter. This case confirms that a stable recombinant chromosome can result from a paracentric inversion. The recombinant was derived by two crossovers, one within the inversion loop and a second outside the inversion loop, between 9q21 and the beginning of the mieotic inversion at 9q22.1. In 87 cells the rec(9) had one Cd-positive primary constriction. In 13 cells the rec(9) had two primary constrictions; in 12 of these cells there was one Cd-positive centromere, and in one of these cells both primary constrictions were Cd-positive. Nuclear projections were observed in 10% of fibroblast interphase cells harvested in situ, suggesting that there was some spindle-fiber activity of the " ***latent*** " ***centromere*** . In situ hybridization with a centromere-specific probe (p82H) and a satellite III probe (L6) revealed no differences between the two C-band regions of the rec(9) and the normal 9 or inverted 9 chromosomes.

L16 ANSWER 14 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 11
AN 1980:264987 BIOSIS
DN PREV198070057483; BA70:57483
TI CD BANDS AND CENTROMERIC FUNCTION IN DICENTRIC CHROMOSOMES.
AU MARASCHIO P [Reprint author]; ZUFFARDI O; CURTO F L
CS IST BIOL GEN GENET MED, UNIV PAVIA, CP 217, I-27100 PAVIA, ITALY
SO Human Genetics, (1980) Vol. 54, No. 2, pp. 265-268.
CODEN: HUGEDQ. ISSN: 0340-6717.
DT Article
FS BA
LA ENGLISH
AB The Cd technique was applied to 2 [human] cases of dicentric attached X chromosomes (XpXp and XqXq) and to cells from an established cell line of tumor origin (MaNo9) in which dicentrics with 2 active centromeres and dicentrics with 1 active and 1 inactive centromere were present. The Cd technique discriminated between active and latent centromeres. True dicentrics and dicentrics with 1 ***latent*** ***centromere*** can coexist within the same cell. The mechanism of centromere inactivation is a phenomenon that is specific to each chromosome and not generalized at the level of the individual cell.

L16 ANSWER 15 OF 16 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN
AN 78026319 EMBASE
DN 1978026319
TI [Partial trisomy 21: trisomy of band 21q22 responsible for Down's syndrome].
FIFTH INTERNATIONAL CONGRESS OF HUMAN GENETICS.
AU Hagemeijer A.; Smit E.M.E.
CS Netherlands
SO (1976) No. 397/- (No. 332).
DT Book
FS 022 Human Genetics
LA English
AB A 6 yr old girl was studied because of retarded intellectual maturation. Her physical and motor development was only slightly delayed. She did not present with a mongoloid phenotype. The facies was rather flat with a wide, often open mouth. Nystagmus was present. The heart was normal. The dermatoglyphs were within the normal range and not at all specific for Down's syndrome. Her karyotype revealed 46 chromosomes with a tandem translocation of 2 chromosomes 21: 46,XX, 21, tan(21;21). G, Q, R and C banding demonstrated a pseudoisodicentric chromosome 21 which appeared symmetrical on either side of band q22. This chromosome can be described as (21)(pter .fwdarw. cen .fwdarw. q22:: q21 .fwdarw. latent cen .fwdarw. pter) according to the nomenclature of the Paris Conference (1971). Satellite association occurred at both ends. The ***centromere*** and the ***latent*** ***centromere*** were demonstrated by C banding; the long arms were duplicated with the exception of band q22 which clearly was not repeated (R banding). The karyotypes of both parents were normal. This observation constitutes strong evidence that trisomy of the distal band of chromosome 21 (band 21q22) is essential for the Down's syndrome phenotype.

L16 ANSWER 16 OF 16 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 12
AN 1976:236525 BIOSIS
DN PREV197662066525; BA62:66525
TI FUSION OF 2 APPARENTLY INTACT HUMAN X CHROMOSOMES.
AU SINHA A K; PATHAK S; NORA J J
SO Human Genetics, (1976) Vol. 32, No. 3, pp. 295-300.
CODEN: HUGEDQ. ISSN: 0340-6717.
DT Article
FS BA
LA Unavailable
AB Cytological studies were presented from a 15 yr old girl with short stature and failure of puberty. Buccal mucosa preparations revealed X-chromatin mass approximately double in size of that of a normal female. Leukocyte metaphases suggested a 2 cell line composition of the patient. One population of cells conformed with 45,X chromosome distribution. The chromosome complement of her other cell line had a modal number of 46. In this cell line a C chromosome was replaced by an exceptionally large submetacentric chromosome. This abnormal element exhibited a late DNA replicating pattern. G-banding study revealed that the abnormal chromosome was produced as a result of fusion involving telomeric ends of long arms of 2 intact X chromosomes. This translocation X was bearing 2 C-banded areas; one around the centromere and the other at the distal end of the long arm. The distal C-band area did not show any evidence for centromeric function. It appears that a ***centromere*** becomes ***latent*** in the presence of another centromere in a translocation bearing 2 total chromosomes. Such a change of state in the additional centromere is vital for the stability of the translocation chromosome.

=> s mar del 10 or mardel 10
L17 17 MAR DEL 10 OR MARDEL 10

=> dup rem l17
PROCESSING COMPLETED FOR L17
L18 9 DUP REM L17 (8 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 9 ANSWERS - CONTINUE? Y/(N):y

L18 ANSWER 1 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:389325 CAPLUS
DN 139:162562
TI Centromeric chromatin pliability and memory at a human neocentromere
AU Craig, Jeffrey M.; Wong, Lee H.; Lo, Anthony W. I.; Earle, Elizabeth; Choo, K. H. Andy
CS Murdoch Childrens Research Institute, Royal Children's Hospital, Melbourne, Victoria, 3052, Australia
SO EMBO Journal (2003), 22(10), 2495-2504
CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English
AB We show that Trichostatin A (TSA)-induced partial histone hyperacetylation

causes a unidirectional shift in the position of a previously defined binding domain for the centromere-specific histone H3 homolog CENP-A at a human neocentromere. The shift of .apprx.320 kb is fully reversible when TSA is removed, but is accompanied by an apparent redn. in the d. of CENP-A per unit length of genomic DNA at the neocentromere. TSA treatment also instigates a reversible abolition of a previously defined major domain of differentially delayed replication timing that was originally established at the neocentromeric site. None of these changes has any measurable deleterious effects on mitosis or neocentromere function. The data suggest pliability of centromeric chromatin in response to epigenetic triggers, and the non-essential nature of the regions of delayed replication for centromere function. Reversibility of the CENP-A-binding position and the predominant region of delayed replication timing following removal of TSA suggest strong memory at the original site of neocentromeric chromatin formation.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 2 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:487757 CAPLUS
DN 137:42666
TI Neocentromere-based human minichromosome construction by telomere-associated chromosomal truncation
IN Choo, Kong-Hong Andy; Wong, Lee Hwa; Saffery, Richard Eric
PA Amrad Operations Pty Ltd, Australia; Murdoch Childrens Research Institute
SO PCT Int. Appl., 61 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002050288	A1	20020627	WO 2001-AU1644	20011220
WO 2002050288	C2	20030807		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002015697	A5	20020701	AU 2002-15697	20011220
EP 1354055	A1	20031022	EP 2001-271443	20011220
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
JP 2004525615	T2	20040826	JP 2002-552165	20011220
US 2004081982	A1	20040429	US 2003-463981	20030617
PRAI AU 2000-2247	A	20001221		
AU 2001-8909	A	20011116		
WO 2001-AU1644	W	20011220		

AB The present invention is directed generally to a defined or isolated nucleic acid mol. encompassing a neocentreomere or a functional deriv. thereof or a latent, synthetic or hybrid form thereof and its use inter alia in developing a range of eukaryotic mini-chromosomes and artificial chromosomes including mammalian (e.g. human) and non-mammalian mini-chromosomes and artificial chromosomes. The present invention further provides a telomere-assocd. chromosome truncation (TACT) approach to develop mini-chromosomes, but is not limited to this approach. It is directed to any truncation approach that produces a neocentromere-contg. mini-chromosome, or any transfection approach using cloned or pre-fabricated DNA that provides neocentromere function in the construction of artificial chromosome. Such mini-chromosomes and artificial chromosomes are useful in a range of genetic therapies. Neocentromeres (NCs) are fully functional centromeres that arise ectopically in noncentromeric regions lacking .alpha.-satellite DNA. Using telomere-assocd. chromosome truncation, the inventors have produced a series of minichromosomes (MiCs) from a ***mardel*** (***10***) marker chromosome contg. a previously characterized human NC. These MiCs range in size from .apprxeq 0.7 to 1.8 Mb and contain single-copy intact genomic DNA from the 10q25 region. Two of these NC-based Mi-Cs (NC-MiCs) appear circular whereas one is linear. All demonstrate stability in both structure and mitotic transmission in the absence of drug selection. Presence of a functional NC is shown by binding a host of key centromere-assocd. proteins. These NC-MiCs provide direct evidence for mitotic segregation function of the NC DNA and represent examples of stable mammalian MiCs lacking centromeric repeats.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 3 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 1
AN 2002:329478 BIOSIS
DN PREV200200329478
TI Construction of neocentromere-based human minichromosomes for gene delivery and centromere studies.
AU Wong, L. H.; Saffery, R.; Choo, K. H. A. [Reprint author]
CS Murdoch Childrens Research Institute, Royal Children's Hospital, Flemington Road, Melbourne, VIC, 3052, Australia
SO Gene Therapy, (June, 2002) Vol. 9, No. 11, pp. 724-726. print.
ISSN: 0969-7128.
DT Article
LA English
ED Entered STN: 12 Jun 2002
Last Updated on STN: 12 Jun 2002
AB Human neocentromeres are fully functional centromeres that arise naturally in non-centromeric regions devoid of alpha-satellite DNA. We have successfully produced a series of minichromosomes by telomere-associated truncation of a marker chromosome ***mardel*** (***10***) containing a neocentromere. The resulting minichromosomes are either linear or circular in nature, and range in size from approximately 650 kb to 2 Mb. These minichromosomes exhibit full centromeric activity, bind to essential centromere proteins, and are mitotically stable over many generations. They provide a useful system for dissecting the functional domains of complex eukaryotic centromeres and as vectors for therapeutic gene delivery.

L18 ANSWER 4 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 2
AN 2001:304117 BIOSIS
DN PREV200100304117
TI Construction of neocentromere-based human minichromosomes by telomere-associated chromosomal truncation.
AU Saffery, Richard; Wong, Lee H.; Irvine, Danielle V.; Bateman, Melissa A.; Griffiths, Belinda; Cutts, Suzanne M.; Cancilla, Michael R.; Cendron, Angela C.; Stafford, Angela J.; Choo, K. H. Andy [Reprint author]
CS Murdoch Children's Research Institute, Royal Children's Hospital, Flemington Road, Melbourne, VIC, 3052, Australia
choo@cryptic.rch.unimelb.edu.au
SO Proceedings of the National Academy of Sciences of the United States of America, (May 8, 2001) Vol. 98, No. 10, pp. 5705-5710. print.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
LA English
ED Entered STN: 27 Jun 2001
Last Updated on STN: 19 Feb 2002
AB Neocentromeres (NCs) are fully functional centromeres that arise ectopically in noncentromeric regions lacking alpha-satellite DNA. Using telomere-associated chromosome truncation, we have produced a series of minichromosomes (MiCs) from a ***mardel*** (***10***) marker chromosome containing a previously characterized human NC. These MiCs range in size from apprxeq0.7 to 1.8 Mb and contain single-copy intact genomic DNA from the 10q25 region. Two of these NC-based Mi-Cs (NC-MiCs) appear circular whereas one is linear. All demonstrate stability in both structure and mitotic transmission in the absence of drug selection. Presence of a functional NC is shown by binding a host of key centromere-associated proteins. These NC-MiCs provide direct evidence for mitotic segregation function of the NC DNA and represent examples of stable mammalian MiCs lacking centromeric repeats.

L18 ANSWER 5 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 3
AN 2001:266965 BIOSIS
DN PREV200100266965
TI A 330 kb CENP-A binding domain and altered replication timing at a human neocentromere.
AU Lo, Anthony W. I.; Craig, Jeffrey M.; Saffery, Richard; Kalitsis, Paul; Irvine, Danielle V.; Earle, Elizabeth; Magliano, Dianna J.; Choo, K. H. Andy [Reprint author]
CS The Murdoch Childrens Research Institute, Royal Children's Hospital, Flemington Road, Melbourne, Victoria, 3052, Australia
choo@cryptic.rch.unimelb.edu.au
SO EMBO (European Molecular Biology Organization) Journal, (April 17, 2001) Vol. 20, No. 8, pp. 2087-2096. print.
CODEN: EMJODG. ISSN: 0261-4189.
DT Article
LA English
ED Entered STN: 6 Jun 2001
Last Updated on STN: 19 Feb 2002
AB Centromere protein A (CENP-A) is an essential centromere-specific histone H3 homologue. Using combined chromatin immunoprecipitation and DNA array analysis, we have defined a 330 kb CENP-A binding domain of a 10q25.3 neocentromere found on the human marker chromosome ***mardel*** (***10***). This domain is situated adjacent to the 80 kb region identified previously as the neocentromere site through lower-resolution immunofluorescence/FISH analysis of metaphase chromosomes. The 330 kb CENP-A binding domain shows a depletion of histone H3, providing evidence for the replacement of histone H3 by CENP-A within centromere-specific nucleosomes. The DNA within this domain has a high AT-content comparable to that of alpha-satellite, a high prevalence of LINEs and tandem repeats, and fewer SINEs and potential genes than the surrounding region. FISH analysis indicates that the normal 10q25.3 genomic region replicates around mid-S phase. Neocentromere formation is accompanied by a replication time lag around but not within the CENP-A binding region, with this lag being significantly more prominent to one side. The availability of fully sequenced genomic markers makes human neocentromeres a powerful model for dissecting the functional domains of complex higher eukaryotic centromeres.

L18 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:761972 CAPLUS
DN 129:340539
TI Neocentromeric DNA sequence from human chromosome 10q25 with uses as artificial chromosome vectors
IN Choo, Kong-Hong Andy; Du Sart, Desiree; Cancilla, Michael Robert
PA Amrad Operations Pty. Ltd., Australia
SO PCT Int. Appl., 540 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9851790	A1	19981119	WO 1998-AU352	19980513
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9873258	A1	19981208	AU 1998-73258	19980513
AU 731572	B2	20010405		
EP 996719	A1	20000503	EP 1998-920396	19980513
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 6265211	B1	20010724	US 1998-78294	19980513
US 2003096398	A1	20030522	US 2000-728552	20001202
PRAI AU 1997-6784	A	19970513		
AU 1997-8791	A	19970826		
US 1998-78294	A1	19980513		
WO 1998-AU352	W	19980513		

AB The present invention is directed generally to an isolated nucleic acid mol. encompassing a neocentromere or a functional deriv. thereof or a latent, synthetic or hybrid form thereof and its use inter alia in developing a range of eukaryotic artificial chromosomes including mammalian (e.g. human) and non-mammalian artificial chromosomes. An unusual human marker chromosome, ***mardel*** (***10***), is identified which is 100% stable in mitotic division both in the original patient and in established fibroblast and transformed lymphoblast cultures. A region of the ***mardel*** (***10***) chromosome was cloned together with the corresponding region from a normal human subject. The nucleic acid mols. cloned contain no substantial .alpha.-satellite repeats yet are mitotically stable. The nucleic acid mols. encompass, therefore, a new form of centromere referred to as a neocentromere. The identification and cloning of a eukaryotic neocentromere without substantial .alpha.-satellite DNA repeat sequences provides a means of generating a range of eukaryotic artificial chromosomes such as mammalian including human artificial chromosomes with uses in genetic therapy, transgenic plant and animal prodn. and recombinant protein prodn. A range of diagnostic reagents is now also obtainable using the cloned neocentromere.
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:181699 CAPLUS
DN 128:304528
TI Direct cloning of human 10q25 neocentromere DNA using transformation-associated recombination (TAR) in yeast
AU Cancilla, Michael R.; Tainton, Kellie M.; Barry, Alyssa E.; Larionov, Vladimir; Kouprina, Natalya; Resnick, Michael A.; Du Sart, Desiree; Choo, K. H. Andy
CS Murdoch Institute Research Birth Defects, Royal Children's Hospital, Parkville, 3052, Australia
SO Genomics (1998), 47(3), 399-404
CODEN: GNMCEP; ISSN: 0888-7543
PB Academic Press
DT Journal
LA English
AB The transformation-assocd. recombination (TAR) procedure allows rapid, site-directed cloning of specific human chromosomal regions as yeast artificial chromosomes (YACs). The procedure requires knowledge of only a single, relatively small genomic sequence that resides adjacent to the chromosomal region of interest. We applied this approach to the cloning of the neocentromere DNA of a marker chromosome that we have previously shown to have originated through the activation of a latent centromere at human chromosome 10q25. Using a unique 1.4-kb DNA fragment as a "hook" in TAR expts., we achieved single-step isolation of the crit. neocentromere DNA region as two stable, 110- and 80-kb circular YACs. For obtaining large quantities of highly purified DNA, these YACs were retrofitted with the yeast-bacteria-mammalian-cells shuttle vector BRV1, electroporated into Escherichia coli DH10B, and isolated as bacterial artificial chromosomes (BACs). Extensive characterization of these YACs and BACs by PCR and restriction analyses revealed that they are identical to the corresponding regions of the normal chromosome 10 and provided further support for the formation of the neocentromere within the marker chromosome through epigenetic activation.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 8 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
DUPLICATE 4
AN 1993:499629 BIOSIS
DN PREV199396123636
TI A functional marker centromere with no detectable alpha-satellite, satellite III, or CENP-B protein: Activation of a latent centromere?.
AU Voullaire, Lucille E.; Slater, Howard R.; Petrovic, Vida; Choo, K. H. Andy [Reprint author]
CS Murdoch Inst., Royal Children's Hosp., Flemington Road, Parkville, Victoria 3052, Australia
SO American Journal of Human Genetics, (1993) Vol. 52, No. 6, pp. 1153-1163.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
LA English
ED Entered STN: 5 Nov 1993
Last Updated on STN: 5 Nov 1993
AB We report the investigation of an unusual human supernumerary marker chromosome 10 designated " ***mar*** ***del*** (***10***)." This marker is present together with two other marker chromosomes in the karyotype of a boy with mild developmental delay. It has a functional centromere at a primary constriction and is mitotically stable. Fluorescence in situ hybridization (FISH) using alpha-satellite and satellite III DNA as probes failed to detect any signal at the primary constriction site. CENP-B protein could not be demonstrated, although the presence of at least some centromeric proteins was confirmed using a CREST antiserum. Consideration of these and other cytogenetic and FISH results supports a mechanism of formation of the ***mar*** ***del*** (***10***) chromosome involving the activation of a latent intercalary centromere at 10q25.

L18 ANSWER 9 OF 9 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1993:499630 BIOSIS
DN PREV199396123637
TI Maternal uniparental disomy for human chromosome 14, due to loss of a chromosome 14 from somatic cells with t(13;14) trisomy 14.
AU Antonarakis, Stylianos E. [Reprint author]; Blouin, Jean-Louis; Maher, Joseph; Avramopoulos, Dimitrios; Thomas, George; Talbot, C. Conover, Jr.
CS CMSC 1003, Johns Hopkins Hosp., 600 North Wolfe St., Baltimore, MD 21287-3914, USA
SO American Journal of Human Genetics, (1993) Vol. 52, No. 6, pp. 1145-1152.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Article
LA English
ED Entered STN: 5 Nov 1993
Last Updated on STN: 5 Nov 1993
AB Uniparental disomy (UPD) for particular chromosomes is increasingly recognized as a cause of abnormal phenotypes in humans. We recently studied in 9-year-old female with a de novo Robertsonian translocation t(13;14), short stature, mild developmental delay, scoliosis, hyperextensible joints, hydrocephalus that resolved spontaneously during the first year of life, and hypercholesterolemia. To determine the parental origin of chromosomes 13 and 14 in the proband, we have studied the genotypes of DNA polymorphic markers due to (GT)n repeats in the patient and her parents' blood DNA. The genotypes of markers D14S43, D14S45, D14S49, and D14S54 indicated maternal UPD for chromosome 14. There was isodisomy for proximal markers and heterodisomy for distal markers, suggesting a recombination event on maternal chromosomes 14. In addition, DNA analysis first revealed sbd and subsequent cytogenetic analysis confirmed sbd that there was mosaic trisomy 14 and 5% of blood lymphocytes. There was normal (biparental) inheritance for chromosome 13, and there was no evidence of false paternity in genotypes of 11 highly polymorphic markers on human chromosome 21. Two cases of maternal UPD for chromosome 14 have previously been reported, one with a familial rob t(13;14) and the other with a t(14;14). There are several similarities among these patients, and a "maternal UPD chromosome 14 syndrome" is emerging; however, the contribution of the mosaic trisomy 14 to the phenotype cannot be evaluated. The study of de novo Robertsonian translocations of the type reported here should reveal both the extent of UPD in these events and the contribution of particular chromosomes involved in certain phenotypes.

=> s human artificial chromosome? or mammal? artificial chromosome?
L19 326 HUMAN ARTIFICIAL CHROMOSOME? OR MAMMAL? ARTIFICIAL CHROMOSOME?

=> s l19 and py<=1997
2 FILES SEARCHED...
L20 72 L19 AND PY<=1997

=> s l20 and CENP
L21 1 L20 AND CENP

=> d bib abs

L21 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1997:221345 BIOSIS
DN PREV199799513061
TI Centromeres, ***CENP*** -B and Tigger too.
AU Kipling, David [Reprint author]; Warburton, Peter E.
CS MRC Hum. Genet. Unit, Western Gen. Hosp., Crewe Rd., Edinburgh EH4 2XU, UK
SO Trends in Genetics, (1997) Vol. 13, No. 4, pp. 141-145.
CODEN: TRGEE2. ISSN: 0168-9525.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997

=> dup rem l20
PROCESSING COMPLETED FOR L20
L22 44 DUP REM L20 (28 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 44 ANSWERS - CONTINUE? Y/(N):y

L22 ANSWER 1 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:416625 CAPLUS
DN 133:39084
TI Artificial chromosomes, uses thereof and methods for preparing artificial chromosomes
IN Hadlaczky, Gyula; Szalay, Aladar A.
PA Chromos Molecular Systems, Inc., Can.; The Biological Research Center of the Hungarian Academy of Sciences
SO U.S., 55 pp., Cont.-in-part of U. S. Ser. No. 629,822, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6077697	A	20000620	US 1996-682080	19960715
US 6025155	A	20000215	US 1996-695191	19960807
CA 2250682	AA	19971030	CA 1997-2250682	19970410 <--
CA 2429724	AA	19971030	CA 1997-2429724	19970410 <--
CA 2429726	AA	19971030	CA 1997-2429726	19970410 <--
WO 9740183	A2	19971030	WO 1997-US5911	19970410 <--
WO 9740183	A3	19980205		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9724512	A1	19971112	AU 1997-24512	19970410 <--
EP 929689	A2	19990721	EP 1997-920284	19970410
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
NZ 331815	A	20000428	NZ 1997-331815	19970410
JP 2000508177	T2	20000704	JP 1997-538116	19970410
NZ 503055	A	20020726	NZ 1997-503055	19970410
NZ 516885	A	20020828	NZ 1997-516885	19970410
US 2001008025	A1	20010712	US 1998-96648	19980612
US 6743967	B2	20040601		
US 2002160970	A1	20021031	US 2001-799462	20010305
US 2003033617	A1	20030213	US 2001-836911	20010417
AU 773728	B2	20040603	AU 2001-38957	20010430
US 2002160410	A1	20021031	US 2002-125767	20020417
US 2003083293	A1	20030501	US 2002-151081	20020516
US 2003108914	A1	20030612	US 2002-219694	20020814
US 2003101480	A1	20030529	US 2002-287313	20021101
JP 2004033209	A2	20040205	JP 2003-29830	20030206
US 2004143861	A1	20040722	US 2004-782129	20040218
US 2004163147	A1	20040819	US 2004-808689	20040324
PRAI US 1996-629822	B2	19960410		
US 1990-521073	B1	19900509		
US 1991-759558	A	19910913		
US 1992-892487	B1	19920603		
US 1993-80097	B1	19930623		
US 1995-375271	B1	19950119		
US 1996-682080	A2	19960715		
US 1996-695191	A	19960807		
US 1996-734344	A1	19961021		
AU 1997-24512	A3	19970410		
CA 1997-2250682	A3	19970410		
JP 1997-538116	A3	19970410		
NZ 1997-503055	A1	19970410		
US 1997-835682	B1	19970410		
WO 1997-US5911	W	19970410		
US 1998-96648	A1	19980612		
US 2000-724693	A1	20001128		
US 2000-724726	A1	20001128		
US 2001-799462	A3	20010305		

AB Methods for prepg. cell lines that contain artificial chromosomes, methods for prepn. of artificial chromosomes, methods for purifn. of artificial chromosomes, methods for targeted insertion of heterologous DNA into artificial chromosomes, and methods for delivery of the chromosomes to selected cells and tissues are provided. Also provided are cell lines for use in the methods, and cell lines and chromosomes produced by the methods. In particular, satellite artificial chromosomes that, except for inserted heterologous DNA, are substantially composed of heterochromatin are provided. Methods for use of the artificial chromosomes, including for gene therapy, prodn. of gene products and prodn. of transgenic plants and animals are also provided. Methods for prepg. cell lines that contain ***mammalian*** ***artificial*** ***chromosomes*** (MACs), methods for prepn. of artificial chromosomes, methods for purifn. of artificial chromosomes, methods for targeted insertion of heterologous DNA into artificial chromosomes, and methods for delivery of the chromosomes to selected cells and tissues are provided. Also provided are cell lines for use in the methods, and cell lines and chromosomes produced by the methods. In particular, satellite artificial chromosomes (SATACs) that, except for inserted heterologous DNA, are substantially composed of heterochromatin are provided; also provided are minichromosomes based on amplification of euchromatin. Methods for use of the artificial chromosomes, including for gene therapy, prodn. of gene products and prodn. of transgenic plants and animals are also provided.
RE.CNT 297 THERE ARE 297 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 2 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:114388 CAPLUS
DN 132:147617
TI Artificial chromosomes, uses thereof and methods for preparing artificial chromosomes
IN Hadlaczky, Gyula; Szalay, Aladar A.
PA Chromos Molecular Systems, Inc., Can.; The Biological Research Center of the Hungarian Academy of Sciences
SO U.S., 59 pp., Cont.-in-part of U.S. Ser. No. 682,080.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6025155	A	20000215	US 1996-695191	19960807
US 6077697	A	20000620	US 1996-682080	19960715
CA 2250682	AA	19971030	CA 1997-2250682	19970410 <--
CA 2429724	AA	19971030	CA 1997-2429724	19970410 <--
CA 2429726	AA	19971030	CA 1997-2429726	19970410 <--
WO 9740183	A2	19971030	WO 1997-US5911	19970410 <--
WO 9740183	A3	19980205		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9724512	A1	19971112	AU 1997-24512	19970410 <--
EP 929689	A2	19990721	EP 1997-920284	19970410
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9708855	A	20000104	BR 1997-8855	19970410
NZ 331815	A	20000428	NZ 1997-331815	19970410
JP 2000508177	T2	20000704	JP 1997-538116	19970410
NZ 503055	A	20020726	NZ 1997-503055	19970410
NZ 516885	A	20020828	NZ 1997-516885	19970410
US 2002160970	A1	20021031	US 2001-799462	20010305
US 2003033617	A1	20030213	US 2001-836911	20010417
AU 773728	B2	20040603	AU 2001-38957	20010430
US 2002160410	A1	20021031	US 2002-125767	20020417
US 2003083293	A1	20030501	US 2002-151081	20020516
US 2003108914	A1	20030612	US 2002-219694	20020814
US 2003101480	A1	20030529	US 2002-287313	20021101
JP 2004033209	A2	20040205	JP 2003-29830	20030206
US 2004143861	A1	20040722	US 2004-782129	20040218
US 2004163147	A1	20040819	US 2004-808689	20040324
PRAI US 1996-629822	B2	19960410		
US 1996-682080	A2	19960715		
US 1990-521073	B1	19900509		
US 1991-759558	A	19910913		
US 1992-892487	B1	19920603		
US 1993-80097	B1	19930623		
US 1995-375271	B1	19950119		
US 1996-682191	A	19960715		
US 1996-695191	A	19960807		
US 1996-734344	A1	19961021		
AU 1997-24512	A3	19970410		
CA 1997-2250682	A3	19970410		
JP 1997-538116	A3	19970410		
NZ 1997-503055	A1	19970410		
US 1997-835682	B1	19970410		
WO 1997-US5911	W	19970410		
US 1998-96648	A1	19980612		
US 2000-724693	A1	20001128		

US 2000-724726 A1 20001128
US 2001-799462 A3 20010305
AB Methods for prepg. cell lines that contain ***mammalian*** ***artificial*** ***chromosomes*** (MACs), methods for prepn. of artificial chromosomes, methods for purifn. of artificial chromosomes, methods for targeted insertion of heterologous DNA into artificial chromosomes, and methods for delivery of the chromosomes to selected cells and tissues are provided. Also provided are cell lines for use in the methods, and cell lines and chromosomes produced by the methods. In particular, satellite artificial chromosomes (SATACs) that, except for inserted heterologous DNA, are substantially composed of heterochromatin are provided; also provided are minichromosomes based on amplification of euchromatin. Methods for use of the artificial chromosomes, including for gene therapy, prodn. of gene products and prodn. of transgenic plants and animals are also provided.
RE.CNT 318 THERE ARE 318 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 3 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:718036 CAPLUS
DN 128:19355
TI methods for prepg. ***mammalian*** ***artificial*** ***chromosomes*** (MACs)
IN Hadlaczky, Gyula; Szalay, Aladar A.
PA Hadlaczky, Gyula, Hung.; Szalay, Aladar A.; American Gene Therapy, Inc.; Biological Research Center of the Hungarian Academy of Sciences; Loma Linda University
SO PCT Int. Appl., 248 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9740183	A2	19971030	WO 1997-US5911	19970410 <--
WO 9740183	A3	19980205		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6077697	A	20000620	US 1996-682080	19960715
US 6025155	A	20000215	US 1996-695191	19960807
AU 9724512	A1	19971112	AU 1997-24512	19970410 <--
EP 929689	A2	19990721	EP 1997-920284	19970410
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9708855	A	20000104	BR 1997-8855	19970410
NZ 331815	A	20000428	NZ 1997-331815	19970410
JP 2000506177	T2	20000704	JP 1997-538116	19970410
AU 773728	B2	20040603	AU 2001-38957	20010430
US 2004143861	A1	20040722	US 2004-782129	20040218

PRAI US 1996-629822 A 19960410
US 1996-682080 A 19960715
US 1996-695191 A 19960807
US 1996-682191 A 19960715
AU 1997-24512 A3 19970410
WO 1997-US5911 W 19970410
US 1998-96648 A1 19980612
AB Methods for prepg. cell lines that contain artificial chromosomes, methods for prepn. of artificial chromosomes, methods for purifn. of artificial chromosomes, methods for targeted insertion of heterologous DNA into artificial chromosomes, and methods for delivery of the chromosomes to selected cells and tissues are provided. Also provided are cell lines for use in the methods, and cell lines and chromosomes produced by the methods. In particular, satellite artificial chromosomes [SATACs] that, except for inserted heterologous DNA, are substantially composed of heterochromatin, are provided. Methods for use of the artificial chromosomes, including for gene therapy, prodn. of gene products and prodn. of transgenic plants and animals are also provided.

L22 ANSWER 4 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:414064 CAPLUS
DN 127:30119
TI ***Mammalian*** ***artificial*** ***chromosomes*** , method for their preparation, and their use for expression of genes in mammalian cells
IN Scheffler, Immo E.
PA Regents of the University of California, USA
SO PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9716533	A1	19970509	WO 1996-US17476	19961029 <--
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				

PRAI US 1995-550717 19951031
AB The present invention provides a ***mammalian*** ***artificial*** ***chromosome*** (MAC), comprising a centromere and a unique cloning site, said MAC contg. less than 0.1% of the DNA present in a normal haploid genome or the mammalian cell from which the centromere was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of prepg. a MAC. In addn., the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC contg. the selectable marker into the cell. The invention also provides a cell contg. a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker. Human X hamster hydrid cells XJM12.1.3 contg. human chromosome 1 minichromosome were irradiated to prep. XEW8.2.3 cells contg. a minichromosome contg. 1-2 million base pairs of DNA from the short arm of chromosome 1. This minichromosome was found to contain the gene for subunit CII-3 of complex II of the mitochondrial electron transport chain. The cDNA for this gene was cloned and sequenced.

L22 ANSWER 5 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 1
AN 1997:320270 BIOSIS
DN PREV199799610758
TI Efficient combination of large DNA in vitro: In gel site specific recombination (IGSSR) of PAC fragments containing alpha satellite DNA and the human HPRT gene locus.
AU Schindelhauer, Dirk [Reprint author]; Cooke, Howard J.
CS Abt. Med. Genet., Kinderpoliklin., Ludwig-Maximilians-Univ., Goethestr. 29, 80336 Muenchen, Germany
SO Nucleic Acids Research, (1997) Vol. 25, No. 11, pp. 2241-2243.
CODEN: NARHAD. ISSN: 0305-1048.
DT Article
LA English
ED Entered STN: 26 Jul 1997
Last Updated on STN: 26 Jul 1997
AB In an attempt to combine a cloned genomic copy of a selectable gene with different cloned centromeric sequences to develop ***mammalian*** ***artificial*** ***chromosomes*** (MAC) we used site specific recombination mediated by purified Cre recombinase acting on the loxP sequence in PAC vector DNA. A new method was required to purify highly concentrated, virtually 100% intact PAC DNA which could be stored for a long period. Here we show the efficient linking of linearized PACs containing alpha satellite DNA from chromosomes X and 17 with sizes of 125 and 140 kb, respectively, to a 95 kb restriction fragment derived from a 175 kb PAC containing the intact human HPRT gene locus.

L22 ANSWER 6 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 2
AN 1997:514740 BIOSIS
DN PREV199799813943
TI The simplicity of complex MACs.
AU Vos, Jean-Michel H.
CS Lineberger Comprehensive Cancer Cent., Univ. N.C. Chapel Hill, Chapel Hill, NC 27599-7295, USA
SO Nature Biotechnology, (1997) Vol. 15, No. 12, pp. 1257-1259.
ISSN: 1087-0156.
DT Article
LA English
ED Entered STN: 10 Dec 1997
Last Updated on STN: 10 Dec 1997
AB The development of ***mammalian*** ***artificial*** ***chromosomes*** (MACs) would be useful for biotechnology and biomedicine, including their use in functional genomics, transgenic animals and gene therapy. By analogy to large cloning systems in microorganisms, MACs may be engineered using endogenous chromosomal elements such as the yeast-based artificial chromosomes (YACs), or exogenous extra-chromosomal components derived from viruses and other cellular parasites such as the bacterial-based artificial chromosomes (BACs) and p1 artificial chromosomes (PACs).

L22 ANSWER 7 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1998:32644 BIOSIS
DN PREV199800032644
TI Chromosomal genetics and molecular genetics: A successful hybridization.
AU Gilgenkrantz, Simone [Reprint author]
CS CHU Nancy, 9 rue Basse, 54330 Clerey/Brenon, France
SO M-S (Medecine Sciences), (Nov., 1997) Vol. 13, No. 11, pp. 1237-1238.
print.
ISSN: 0767-0974.
DT Article
Editorial
LA French
ED Entered STN: 14 Jan 1998
Last Updated on STN: 14 Jan 1998

L22 ANSWER 8 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:254189 CAPLUS
TI ***Human*** ***artificial*** ***chromosomes*** : Providing a little stability

AU Warburton, Peter E.; Kipling, David
CS Inst. Cell and Molecular Biol., Univ. Edinburgh, Edinburgh, EH9 3JR, UK
SO Nature (London) (***1997***), 386(6625), 553-555
CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB Unavailable
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 9 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:287855 CAPLUS
TI ***Human*** ***artificial*** ***chromosomes*** constructed
AU Anon.
SO Nature Biotechnology (***1997***), 15(5), 400
CODEN: NABIF9; ISSN: 1087-0156
PB Nature Publishing Co.
DT Journal; News Announcement
LA English
AB Unavailable

L22 ANSWER 10 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1998:112012 BIOSIS
DN PREV199800112012
TI Humanizing the yeast telomerase template gene TLC1.
AU Liu, P. P.; Moskowitz, N.; Rosenfeld, M.; Henning, K. A.
CS National Human Genome Res. Inst., NIH, Bethesda, MD, USA
SO American Journal of Human Genetics, (Oct., 1997) Vol. 61, No. 4 SUPPL., pp. A357. print.
Meeting Info.: 47th Annual Meeting of the American Society of Human Genetics. Baltimore, Maryland, USA. October 28-November 1, 1997.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Mar 1998
Last Updated on STN: 3 Mar 1998

L22 ANSWER 11 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1998:112003 BIOSIS
DN PREV199800112003
TI Production of functional ***human*** ***artificial*** ***chromosomes*** by the modification of YACs containing human centromeric DNA.
AU Henning, K. A.; Novotny, E. A.; Compton, S. T.; Statham, V.; Liu, P. P.; Rosenfeld, M. A.
CS National human Genome Res. Inst., NIH, Bethesda, MD, USA
SO American Journal of Human Genetics, (Oct., 1997) Vol. 61, No. 4 SUPPL., pp. A355. print.
Meeting Info.: 47th Annual Meeting of the American Society of Human Genetics. Baltimore, Maryland, USA. October 28-November 1, 1997.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LA English
ED Entered STN: 3 Mar 1998
Last Updated on STN: 3 Mar 1998

L22 ANSWER 12 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 3
AN 1997:203821 BIOSIS
DN PREV199799503024
TI Formation of de novo centromeres and construction of first-generation human artificial microchromosomes.
AU Harrington, John J.; Van Bokkelen, Gil; Mays, Robert W.; Gustashaw, Karen; Willard, Huntington F. [Reprint author]
CS Dep. Genetics, Case Western Reserve Univ. Sch. Med., Univ. Hosp., Cleveland, OH 44106, USA
SO Nature Genetics, (1997) Vol. 15, No. 4, pp. 345-355.
ISSN: 1061-4036.
DT Article
LA English
ED Entered STN: 12 May 1997
Last Updated on STN: 12 May 1997
AB We have combined long synthetic arrays of alpha satellite DNA with telomeric DNA and genomic DNA to generate artificial chromosomes in human HT1080 cells. The resulting linear microchromosomes contain exogenous alpha satellite DNA, are mitotically and cytogenetically stable in the absence of selection for up to six months in culture, bind centromere proteins specific for active centromeres, and are estimated to be 6-10 megabases in size, approximately one-fifth to one-tenth the size of endogenous human chromosomes. We conclude that this strategy results in the formation of de novo centromere activity and that the microchromosomes so generated contain all of the sequence elements required for stable mitotic chromosome segregation and maintenance. This first-generation system for the construction of ***human*** ***artificial*** ***chromosomes*** should be suitable for dissecting the sequence requirements of human centromeres, as well as developing constructs useful for therapeutic applications.

L22 ANSWER 13 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 4
AN 1997:453890 BIOSIS
DN PREV199799753093
TI ***Mammalian*** ***artificial*** ***chromosomes*** and chromosome transgenics.
AU Huxley, Clare
CS Dep. Biochem. Mol. Genet., Imperial Coll. Sch. Med. at St. Mary's, Norfolk Place, London W2 1PG, UK
SO Trends in Genetics, (1997) Vol. 13, No. 9, pp. 345-347.
CODEN: TRGEE2. ISSN: 0168-9525.
DT Article
LA English
ED Entered STN: 27 Oct 1997
Last Updated on STN: 27 Oct 1997

L22 ANSWER 14 OF 44 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 5
AN 97102609 EMBASE
DN 1997102609
TI ***Human*** ***artificial*** ***chromosomes*** get real.
AU Rosenfeld M.A.
CS M.A. Rosenfeld, Laboratory of Gene Transfer, National Human Genome Research Inst., National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892, United States. melis@nhgri.nih.gov
SO Nature Genetics, (1997) 15/4 (333-335).
Refs: 29
ISSN: 1061-4036 CODEN: NGENEC
CY United States
DT Journal; General Review
FS 005 General Pathology and Pathological Anatomy
022 Human Genetics
029 Clinical Biochemistry
LA English

L22 ANSWER 15 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 6
AN 1997:438961 BIOSIS
DN PREV199799738164
TI Human centromeric DNAs.
AU Lee, C.; Wevrick, R.; Fisher, R. B.; Ferguson-Smith, M. A. [Reprint author]; Lin, C. C.
CS Dep. Pathol., Univ. Cambridge, Tennis Court Road, Cambridge CB2 1QP, UK
SO Human Genetics, (1997) Vol. 100, No. 3-4, pp. 291-304.
CODEN: HUGEDQ. ISSN: 0340-6717.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997
AB Human centromeres have been extensively studied over the past two decades.
Consequently, more is known of centromere structure and organization in humans than in any other higher eukaryote species. Recent advances in the construction of a human (or ***mammalian***) ***artificial*** ***chromosome*** have fostered increased interest in determining the structure and function of fully functional human centromeres. Here, we present an overview of currently identified human centromeric repetitive DNA families: their discoveries, molecular characterization, and organization with respect to other centromeric repetitive DNA families. A brief examination of some functional based studies is also included.

L22 ANSWER 16 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1997:221345 BIOSIS
DN PREV199799513061
TI Centromeres, CENP-B and Tigger too.
AU Kipling, David [Reprint author]; Warburton, Peter E.
CS MRC Hum. Genet. Unit, Western Gen. Hosp., Crewe Rd., Edinburgh EH4 2XU, UK
SO Trends in Genetics, (1997) Vol. 13, No. 4, pp. 141-145.
CODEN: TRGEE2. ISSN: 0168-9525.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997

L22 ANSWER 17 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 7
AN 1997:500588 BIOSIS
DN PREV199799799791
TI ***Mammalian*** ***artificial*** ***chromosomes*** -vectors for

somatic gene therapy.
AU Ascenzioni, F.; Donini, P.; Lipps, H. J. [Reprint author]
CS Inst. Zellbiol., Univ. Witten/Herdecke, Stockumer Str. 10, D-58448 Witten, Germany
SO Cancer Letters, (1997) Vol. 118, No. 2, pp. 135-142.
CODEN: CALEDQ. ISSN: 0304-3835.
DT Article
LA English
ED Entered STN: 21 Nov 1997
Last Updated on STN: 21 Nov 1997
AB ***Mammalian*** ***artificial*** ***chromosomes*** might prove to be useful vectors for somatic gene therapy. The functional elements of such an artificial chromosome are telomeres, a centromere and a replication origin. Recent progress in the characterization of these functional elements of the eukaryotic chromosome will be described. Attempts to construct artificial chromosomes for mammalian cells and their use for somatic gene therapy are discussed.

L22 ANSWER 18 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:735745 CAPLUS
DN 126:15259
TI Physical mapping by pulsed-field gel electrophoresis
AU Maule, John
CS MRC Human Genetics Unit, Western General Hospital, Edinburgh, UK
SO Methods in Molecular Biology (Totowa, New Jersey) (***1997***), 68(Gene Isolation and Mapping Protocols), 93-121
CODEN: MMBIED; ISSN: 1064-3745
PB Humana
DT Journal
LA English
AB Long-range phys. mapping relies on the correct use of appropriate restriction enzymes, taking account of the base compn. and methylation status of the organism, to generate large fragments that can link together probes for mapping purposes to detect chromosome rearrangements. Before the availability of pulsed-field gel electrophoresis (PFGE), longe range phys. mapping was limited by the cloning capacity of .gamma. and cosmid vectors. The ability to generate and sep. large DNA fragments has allowed a new approach tp phys. mapping. Protocols involving cloning long stretches of genomic DNA into yeast artificial chromosomes (YACs) and the technol. difficulties assocd. with the creation of ***mammalian*** ***artificial*** ***chromosomes*** (MACs) are being addressed. Conventional agarose gel electrophoresis can sep. DNA mols. no greater than about 50kb, whereas PFGE has resolved DNA as large as 12 Mb. The basis of the technique relies on a elec. field that regularly changes in orientation relative to the DNA-contg. gel. Attempts to overcome the inherent difficulties in transferring large DNA mols. to hybridizing membranes have led to the development of protocols for drying and hybridizing pulsed-field gels. Protocols foe blotting gels and prepg. and hybridizing dried agarose gels are provided.

L22 ANSWER 19 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1998:109925 BIOSIS
DN PREV199800109925
TI Generation and characterization of ***human*** ***artificial*** ***chromosomes*** in human and mouse cells.
AU Willard, H. F. [Reprint author]; Harrington, J.; Mays, W.; Sherf, B.; Vanbokkelen, G.
CS Case Western Reserve Univ., Cleveland, OH, USA
SO American Journal of Human Genetics, (Oct., 1997) Vol. 61, No. 4 SUPPL., pp. A3. print
Meeting Info.: 47th Annual Meeting of the American Society of Human Genetics. Baltimore, Maryland, USA. October 28-November 1, 1997.
CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 3 Mar 1998
Last Updated on STN: 3 Mar 1998

L22 ANSWER 20 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:121411 CAPLUS
DN 126:127860
TI Synthetic mammalian chromosome and methods for construction
IN Van Bokkelen, Gil B.; Harrington, John J.; Willard, Huntington F.
PA Van Bokkelen, Gil B., USA; Harrington, John J.; Willard, Huntington F.
SO PCT Int. Appl., 103 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9640965	A1	19961219	WO 1996-US10248	19960607 <--
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA				
US 5695967	A	19971209	US 1995-487989	19950607 <--
US 6348353	B1	20020219	US 1996-643554	19960506
AU 9662781	A1	19961230	AU 1996-62781	19960607 <--
AU 724695	B2	20000928		
EP 832273	A1	19980401	EP 1996-921588	19960607
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9608586	A	19981229	BR 1996-8586	19960607
JP 11507540	T2	19990706	JP 1996-502261	19960607
AU 761362	B2	20030605	AU 2000-71442	20001031
PRAI US 1995-487989	A	19950607		
US 1996-643554	A	19960506		
AU 1996-62781	A3	19960607		
WO 1996-US10248	W	19960607		

AB The invention relates to the field of gene therapy, gene expression, and vectors for these uses. In particular, the invention relates to a method for producing structurally intact large repeating units of DNA, esp. useful for the stable cloning of alpha satellite DNA, and to the development and use of a synthetic or artificial chromosome for gene expression and gene therapy in mammals, and esp. humans. The invention allows the controlled construction of stable synthetic or artificial chromosomes constructed from isolated segments of purified DNA. Functional minimal segments preferably include centromeric DNA, telomeric DNA, and genomic DNA. The artificial chromosome performs the essential chromosomal functions of naturally-occurring chromosomes so as to permit the chromosome to function as an effective vector for gene therapy. A directional cloning strategy allowed the creation of .alpha.-satellite arrays of known compn. and structure. This technique allowed the prodn. of contiguous, uninterrupted Y .alpha.-satellite arrays up to 736 kb in length. Mitotically stable synthetic chromosomes were created by transfecting large .alpha.-satellite arrays (derived from either chromosome Y or from chromosome 17), telomeric DNA, and genomic DNA together into HT1080 cells.

L22 ANSWER 21 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 8
AN 1996:388808 BIOSIS
DN PREV199699111164
TI ***Mammalian*** ***artificial*** ***chromosomes*** .
AU Brown, William [Reprint author]; Heller, Raoul; Loupart, Marie-Louise; Shen, Ming-Hong; Chand, Aarti
CS CRC Chromosome Mol. Biol. Group, Biochem. Dep., Oxford Univ., South Parks Road, Oxford OX1 3QU, UK
SO Current Opinion in Genetics and Development, (1996) Vol. 6, No. 3, pp. 281-288.
ISSN: 0959-437X.
DT Article
LA English
ED Entered STN: 3 Sep 1996
Last Updated on STN: 3 Sep 1996

L22 ANSWER 22 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 9
AN 1997:110025 BIOSIS
DN PREV199799409228
TI ***Mammalian*** ***artificial*** ***chromosomes*** : A review.
AU Sgaramella, Vittorio; Eridani, Sandro
CS ITBA, Natl. Res. Council, Via Ampere 56, Milano, Italy
SO Cytotechnology, (1996) Vol. 21, No. 3, pp. 253-261.
ISSN: 0920-9069.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 10 Mar 1997
Last Updated on STN: 10 Mar 1997
AB A ***mammalian*** ***artificial*** ***chromosome*** (MAC) may be assembled through the juxtapposition of three kinds of DNA elements: a centromere, several DNA replication origins, and two telomeric repeats. The resulting structure should be able to carry and express one or more selected genes (transgenes), introduced for specific purposes. The minimal length is unknown, but may be of several Mb. Of its basic elements, the telomeres may present lesser problems, in view of their simple composition and organization. Centromeres could be an issue, given their many unknowns. Mammalian DNA replication origins are at present poorly characterized, but it is expected that at least one may be contained within the MAC components, especially the transgene. Their overall assembly may require a combination of in vivo and in vitro approaches. A promising strategy aims at constructing two telomeric arms of a MAC, one of which may include the transgene. The two novel arms could acquire a functional centromere through recombination with the two arms of a resident chromosome. Alternatively, if the two telomeric constructs are also endowed with properly placed and oriented centromeric sequences, a centromere may be rescued in vivo by homologous recombination with the external parts of the centromere of the resident chromosome. Positive selection for the artificial arms and counterselection against the resident arms should facilitate the assembly process. The assembly of such construct would not change the ploidy number of the host cell. After loading of a transgene, however, the resulting MAC may be isolated and transferred into an expression cell, where it may represent a novel chromosomal element. In this case untoward effects to the host cell may derive from an ensuing dosage effect for the transgene(s) rather than from the presence of a MAC per se. A MAC may contribute to a deeper

understanding of the structural requirements for chromosomal function and evolution as well as the mechanism of chromatin formation. It should also help in the development of second generation vectors for transfer of Mb-long DNA sequences, as required for properly regulated mammalian gene function as well as, possibly, for therapy.

L22 ANSWER 23 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:305793 CAPLUS
DN 129:104706
TI Development of ***mammalian*** ***artificial*** ***chromosome*** vectors: prospects for somatic gene transfer
AU Larin, Zoia
CS Institute of Molecular Medicine, John Radcliffe Hospital, University of Oxford, Oxford, OX3 9DU, UK
SO Gene Therapy (***1998***), 113-126. Editor(s): Lemoine, Nicholas R.; Cooper, David N. Publisher: Bios Scientific Publishers, Oxford, UK. CODEN: 66AOAO
DT Conference; General Review
LA English
AB A review with 56 refs. on eukaryotic chromosome structure and function as a basis for understanding the requirements for constructing ***mammalian*** ***artificial*** ***chromosomes*** (MACs) for gene transfer and gene therapy. Topics include: properties of a functional chromosome in the eukaryotic cell cycle; linear yeast artificial chromosomes; components required for ***human*** ***artificial*** ***chromosomes*** ; strategies for constructing MACs; and prospects of MACs for somatic gene transfer.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 24 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 10
AN 1996:484437 BIOSIS
DN PREV199699199693
TI Analysis of extrachromosomal structures containing human centromeric alphoid satellite DNA sequences in mouse cells.
AU Taylor, Stephen S. [Reprint author]; Larin, Zoia; Tyler-Smith, Chris
CS Dep. Cell Biol., Harvard Med. Sch., 240 Longwood Ave., Boston, MA 02115, USA
SO Chromosoma (Berlin), (1996) Vol. 105, No. 2, pp. 70-81. CODEN: CHROAU. ISSN: 0009-5915.
DT Article
LA English
ED Entered STN: 24 Oct 1996
Last Updated on STN: 24 Oct 1996
AB Yeast artificial chromosomes (YACs) spanning the centromeric region of the human Y chromosome were introduced into mouse LA-9 cells by spheroplast fusion in order to determine whether they would form ***mammalian*** ***artificial*** ***chromosomes*** . In about 50% of the cell lines generated, the YAC DNA was associated with circular extrachromosomal structures. These episomes were only present in a proportion of the cells, usually at high copy number, and were lost rapidly in the absence of selection. These observations suggest that, despite the presence of centromeric sequences, the structures were not segregating efficiently and thus were not forming artificial chromosomes. However, extrachromosomal structures containing alphoid DNA appeared cytogenetically smaller than those lacking it, as long as yeast DNA was also absent. This suggests that alphoid DNA can generate the condensed chromatin structure at the centromere.

L22 ANSWER 25 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:555270 BIOSIS
DN PREV199699277626
TI Transfer of the full-size DMD-gene to mammalian cells with the use of a putative ***mammalian*** ***artificial*** ***chromosome*** .
AU Heus, J. J.; Wiersma, A. J.; De Meijer, E.; Van Ommen, G. J. B.; Den Dunnen, J. T.
CS Leiden University, Dep. Human Genet., Leiden, Netherlands
SO American Journal of Human Genetics, (1996) Vol. 59, No. 4 SUPPL., pp. A56. Meeting Info.: 46th Annual Meeting of the American Society of Human Genetics. San Francisco, California, USA. October 29-November 2, 1996. CODEN: AJHGAG. ISSN: 0002-9297.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Slide)
LA English
ED Entered STN: 13 Dec 1996
Last Updated on STN: 13 Dec 1996

L22 ANSWER 26 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:292823 BIOSIS
DN PREV199699015179
TI Mammalian telomeres and chromosome fragmentation.
AU Farr, Christine J.
CS Dep. Genet., Univ. Cambridge, Downing St., Cambridge CB2 3EH, UK
SO Seminars in Cell and Developmental Biology, (1996) Vol. 7, No. 1, pp. 41-48. ISSN: 1084-9521.
DT Article
LA English
ED Entered STN: 2 Jul 1996
Last Updated on STN: 2 Jul 1996

L22 ANSWER 27 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1996:355263 BIOSIS
DN PREV199699077619
TI Transfer of the entire DMD-gene to mammalian cells with the use of putative ***mammalian*** ***artificial*** ***chromosome*** .
AU Heus, Joris; Wiersma, A.; De Meijer, E.; Van Ommen, G. J.; Den Dunnen, J.
CS Leiden Univ., Dep. Human Genet., Leiden, Netherlands
SO European Journal of Human Genetics, (1996) Vol. 4, No. SUPPL. 1, pp. 8. Meeting Info.: 28th Annual Meeting of the European Society of Human Genetics. London, England, UK. April 11-13, 1996. ISSN: 1018-4813.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 5 Aug 1996
Last Updated on STN: 5 Aug 1996

L22 ANSWER 28 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:76579 CAPLUS
DN 124:108957
TI Functional centromere elements derived from mammalian chromosomes for use in the construction of ***mammalian*** ***artificial*** ***chromosome*** vectors
IN Brown, William
PA Cancer Research Campaign Technology Ltd., UK
SO PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9532297	A1	19951130	WO 1995-GB1195	19950525 <--
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9525343	A1	19951218	AU 1995-25343	19950525 <--
ZA 9504300	A	19960124	ZA 1995-4300	19950525 <--
PRAI GB 1994-10446		19940525		
WO 1995-GB1195		19950525		

AB The isolation of functional elements of mammalian centromeres for use in the construction of ***mammalian*** ***artificial*** ***chromosomes*** using telomere-directed chromosome fragmentation techniques is described for use in, for instance for application in gene therapy and animal gene transfer. These vectors are capable of replication and segregation during cell cycle, and are of a size that can be resolved using gel electrophoresis. Suitable fragments are derived from the human Y chromosome. The generation of truncated human Y-chromosomes that are stable in mitosis is demonstrated.

L22 ANSWER 29 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 11
AN 1996:35615 BIOSIS
DN PREV199698607750
TI Generation of a human X-derived minichromosome using telomere-associated chromosome fragmentation.
AU Farr, Christine J. [Reprint author]; Bayne, Rosemary A. L.; Kipling, David; Mills, Walter; Critcher, Ricky; Cooke, Howard J.
CS Dep. Genet., Univ. Cambridge, Downing St., Cambridge CB2 3EH, UK
SO EMBO (European Molecular Biology Organization) Journal, (1995) Vol. 14, No. 21, pp. 5444-5454. CODEN: EMJODG. ISSN: 0261-4189.
DT Article
LA English
ED Entered STN: 26 Jan 1996
Last Updated on STN: 26 Jan 1996
AB A linear ***mammalian*** ***artificial*** ***chromosome*** vector will require at least three functional elements: a centromere, two telomeres and replication origins. One route to generate such a vector is by the fragmentation of an existing chromosome. We have previously described the use of cloned telomeric DNA to generate and stably rescue truncated derivatives of a human X chromosome in a somatic cell hybrid. Further rounds of telomere-associated chromosome fragmentation have now been used to engineer a human X-derived minichromosome. This minichromosome is estimated to be lt 10 Mb in size. In situ hybridization and molecular analysis reveal that the minichromosome has a linear structure, with two introduced telomere constructs flanking a 2.5 Mb a-satellite array. The highly truncated chromosome also retains some chromosome-specific DNA, originating from Xp11.21. There is no

significant change in the mitotic stability of the minichromosome as compared with the X chromosome from which it was derived.

L22 ANSWER 30 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1996:1192 BIOSIS
DN PREV199698573327
TI Gene therapy: The artificial may improve the natural (as for chromosomes).
AU Sgaramella, Vittorio
CS Dip. Biol. Cell., Univ. Calabria, Arcavacata di Rende, CS, Italy
SO Biology International, (1995) Vol. 0, No. SPEC. ISSUE 33, pp. 25-27.
Meeting Info.: Symposium on Uniqueness and Universality in a Biological World. Paris, France. January 10-12, 1995.
CODEN: BYILDJ. ISSN: 0253-2069.
DT Conference; (Meeting)
Conference; (Meeting Paper)
LA English
ED Entered STN: 4 Jan 1996
Last Updated on STN: 4 Jan 1996

L22 ANSWER 31 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1996:98702 BIOSIS
DN PREV199698670837
TI Gene therapy with ***mammalian*** ***artificial*** ***chromosomes*** .
AU Heus, Joris J.; Wiersma, Annette J.; Van Ommen, Gert-Jan B.; Den Dunnen, Johan T.
CS Leiden Univ., Dep. Human Genetics, Wassenaarseweg 72, 2333 AL Leiden, Netherlands
SO Gene Therapy, (1995) Vol. 2, No. SUPPL. 1, pp. S9.
Meeting Info.: Third Meeting of the European Working Group of Human Gene Transfer and Therapy. Barcelona, Spain. November 17-20, 1995.
ISSN: 0969-7128.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 4 Mar 1996
Last Updated on STN: 4 Mar 1996

L22 ANSWER 32 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1996:98675 BIOSIS
DN PREV199698670810
TI Potential of ***mammalian*** ***artificial*** ***chromosomes*** for gene therapy.
AU Huxley, Clare; Manson, Ania; Simpson, Kaetrin; Vassaux, Georges
CS St. Mary's Hosp. Med. Sch., Imperial Coll., London, UK
SO Gene Therapy, (1995) Vol. 2, No. SUPPL. 1, pp. S2
Meeting Info.: Third Meeting of the European Working Group of Human Gene Transfer and Therapy. Barcelona, Spain. November 17-20, 1995.
ISSN: 0969-7128.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 4 Mar 1996
Last Updated on STN: 4 Mar 1996

L22 ANSWER 33 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 12
AN 1994:482716 BIOSIS
DN PREV199497495716
TI Stringent sequence requirements for the formation of human telomeres.
AU Hanish, John P.; Yanowitz, Judith L.; De Lange, Titia [Reprint author]
CS The Rockefeller Univ., 1230 York Ave., New York, NY 10021, USA
SO Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 19, pp. 8861-8865.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
LA English
ED Entered STN: 9 Nov 1994
Last Updated on STN: 10 Nov 1994
AB In human cells, transfection of telomeric T-2AG-3 repeats induces the formation of functional telomeres at previously interstitial sites. We report that telomere formation has stringent sequence requirements. While (T-2AG-3)-n telomere seeds formed telomeres in apprxeq 70% of the transfected cells, five T-2AG-3-related heterologous telomeric DNAs seeded new telomeres in lt 5% of the transfectants. Telomere formation did not correlate with the ability of human telomerase to elongate telomeric sequences in vitro. Homologous recombination is probably also not involved because a (T-2AG-3)-n telomere seed with nontelomeric DNA at 160-bp intervals formed new telomeres frequently. Instead, the sequence dependence of telomere formation matched the in vitro binding requirements for the mammalian T-2AG-3 repeat binding factor (TRF). Human TRF failed to bind ineffective heterologous telomere seeds and had a 4-fold lower affinity for (T-2AG-5)-2T-2AG-3 repeats, which seeded telomeres with reduced frequency. The results suggest that telomere seeds interact with TRF and predict that ***mammalian*** ***artificial*** ***chromosomes*** will require wild-type telomeric repeats at, or near, their termini.

L22 ANSWER 34 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 13
AN 1995:18064 BIOSIS
DN PREV199598032364
TI Recombination during transformation as a source of chimeric ***mammalian*** ***artificial*** ***chromosomes*** in yeast (YACs).
AU Larionov, V. [Reprint author]; Kouprina, N.; Nikolaishvili, N.; Resnick, M. A.
CS Inst. Cytol., Russian Acad. Sci., St. Petersburg, Russia
SO Nucleic Acids Research, (1994) Vol. 22, No. 20, pp. 4154-4162.
CODEN: NARHAD. ISSN: 0305-1048.
DT Article
LA English
ED Entered STN: 11 Jan 1995
Last Updated on STN: 11 Jan 1995
AB Mammalian DNAs cloned as artificial chromosomes in yeast (YACs) frequently are chimeras formed between noncontiguous DNAs. Using pairs of human and mouse YACs we examined the contribution of recombination during transformation or subsequent mitotic growth to chimeric YAC formation. The DNA from pairs of yeast strains containing homologous or heterologous YACs was transformed into a third strain under conditions typical for the development of YAC libraries. One YAC was selected and the presence of the second was then determined. Co-penetration of large molecules, as deduced from co-transformation of markers identifying the different YACs, was gt 50%. In approximately half the cells receiving two homologous YACs, the YACs had undergone recombination. Co-transformation depends on recombination since it was reduced nearly 10-fold when the YACs were heterologous. While mitotic recombination between homologous YACs is nearly 100-fold higher than for yeast chromosomes, the level is still much lower than observed during transformation. To investigate the role of commonly occurring Alu repeats in chimera formation, spheroplasts were transformed with various human YACs and an unselected DNA fragment containing an Alu at one end and a telomere at the other. When unbroken YACs were used, between 1 and 6% of the selected YACs could incorporate the fragment as compared to 49% when the YACs were broken. We propose that Alu's or other commonly occurring repeats could be an important source of chimeric YACs. Since the frequency of chimeras formed between YACs or a YAC and an Alu-containing fragment was reduced when a rad52 mutant was the recipient and since intraYAC deletions are reduced, rad52 and possibly other recombination-deficient mutants are expected to be useful for YAC library development.

L22 ANSWER 35 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 14
AN 1994:498814 BIOSIS
DN PREV199497511814
TI Addition of functional human telomeres to YACs.
AU Taylor, Stephen S. [Reprint author]; Larin, Zoia; Smith, Chris Tyler
CS CRC chromosome Molecular Biol. Group, Dep. Biochem., Univ. Oxford, South Parks Road, Oxford OX1 3QU, UK
SO Human Molecular Genetics, (1994) Vol. 3, No. 8, pp. 1383-1386.
ISSN: 0964-6906.
DT Article
LA English
ED Entered STN: 28 Nov 1994
Last Updated on STN: 28 Nov 1994
AB Linear ***mammalian*** ***artificial*** ***chromosomes*** (MACs) will require functional telomeres, a centromere and the ability to replicate autonomously. We are investigating the possibility of developing MACs from yeast artificial chromosomes (YACs). Retrofitting vectors have been constructed to replace YAC telomeres with cloned human telomeric DNA. A modified YAC was introduced into mammalian cells by spheroplast fusion and the frequency with which the retrofitted human telomeric DNA seeded the formation of a new telomere was determined by Bal31 digestion and cytogenetic analysis. The telomere adjacent to the selectable marker gene was functional in 5/46 clones (11%) while the telomere 200 kb away at the other end of the YAC was functional in 1/46 clones (2%). These results indicate that despite the in vivo modification of the end of the telomere by the addition of yeast sequences, human telomeres will function at a high enough frequency to allow the construction of MACs by this route.

L22 ANSWER 36 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN DUPLICATE 15
AN 1994:345999 BIOSIS
DN PREV199497358999
TI Sandwiching of a gene within 12 kb of a function telomere and alpha satellite does not result in silencing.
AU Bayne, Rosemary A. L. [Reprint author]; Broccoli, Dominique; Taggart, Mary H.; Thomson, Eric J.; Farr, Christie J.; Cooke, Howard J.
CS MRC Human Genetics Unit, Western General Hosp., Crewe Road, Edinburgh EH4
2XU, UK
SO Human Molecular Genetics, (1994) Vol. 3, No. 4, pp. 539-546.
ISSN: 0964-6906.
DT Article
LA English

OS Genbank-L15279; Genbank-L15281; Genbank-L15283
ED Entered STN: 8 Aug 1994
Last Updated on STN: 1 Sep 1994
AB Pericentric heterochromatin and telomeres have been shown to be capable of repressing the expression of genes located in close proximity. The effect of adjacent structural sequences on gene expression will be important in the design of ***mammalian*** ***artificial*** ***chromosomes*** . In the process of using telomere-containing constructs to generate a deletion panel of the long arm of the human X chromosome, several cell lines were produced which appeared by in situ hybridization to be broken in Xq at or near the centromere. After analysis of end clones rescued from these cell lines, only two produced data consistent with breaks in the alpha satellite array without accompanying rearrangements. The mitotic stability of an X chromosome, with at least 750 kb of the alpha satellite array deleted, was compared to controls where the alpha satellite array remained intact. No significant change in the stability of the chromosome was observed, suggesting that the truncated chromosome has a fully functional mitotic centromere. There was no detectable change in the expression of the hygromycin resistance gene, which is located between a functional centromere and telomere, in this cell line. This study indicates that structural elements flanking a mammalian selectable marker do not result in silencing.

L22 ANSWER 37 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:239235 CAPLUS
DN 122:307560
TI Human artificial episomal chromosomes for cloning large DNA fragments in human cells. [Erratum to document cited in CA121:197076]
AU Sun, Tian-Qiang; Fenstermacher, David A.; Vos, Jean-Michel H.
CS Dep. Biochem. Biophysics, Univ. North Carolina, Chapel Hill, NC, 27599, USA
SO Nature Genetics (***1994***), 8(4), 410
CODEN: NGENEC; ISSN: 1061-4036
PB Nature Publishing Co.
DT Journal
LA English
AB The errors were not reflected in the abstr. or the index entries.

L22 ANSWER 38 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1994:390529 BIOSIS
DN PREV199497403529
TI YACs, BACs, PACs and MACs: Artificial chromosomes as research tools.
AU Monaco, Anthony P. [Reprint author]; Larin, Zoia
CS Imperial Cancer Res. Fund Lab., Inst. Mol. Med., John Radcliffe Hosp., Headington, Oxford OX3 9DU, UK
SO Trends in Biotechnology, (1994) Vol. 12, No. 7, pp. 280-286.
CODEN: TRBIDM. ISSN: 0167-7799.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 14 Sep 1994
Last Updated on STN: 14 Sep 1994

L22 ANSWER 39 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 16
AN 1994:482565 BIOSIS
DN PREV199497495565
TI ***Mammalian*** ***artificial*** ***chromosomes*** : A new tool for gene therapy.
AU Huxley, Clare
CS Dep. Biochem. Mol. Genetics, St. Mary's Hosp. Med. Sch., Norflok Place, London W2 1PG, UK
SO Gene Therapy, (1994) Vol. 1, No. 1, pp. 7-12.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 9 Nov 1994
Last Updated on STN: 9 Nov 1994
AB Effective therapy by in vivo delivery of DNA requires efficient delivery, long-term maintenance of the DNA that is delivered and physiological levels of expression of the therapeutic gene. Full levels of physiologically controlled expression can be obtained after transfer of intact genes on fragments of DNA hundreds of kilobases in size, as has been demonstrated by the transfer of yeast artificial chromosomes into transgenic mice. Long-term maintenance of input DNA could be achieved if the DNA carried replication origins, a centromere and telomeres to allow maintenance and segregation in mammalian cells, and there has been recent progress towards cloning these elements. These features could be combined as a ***mammalian*** ***artificial*** ***chromosome*** which would confer full levels of controlled expression as well as being maintained in any cell into which it was introduced. Methods which would allow delivery of such large fragments of DNA include liposomes and receptor-mediated uptake, both of which have been shown to work in vivo, making such large constructs potentially applicable for use in gene therapy.

L22 ANSWER 40 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AN 1993:350978 BIOSIS
DN PREV199345034403
TI Gene therapy for cystic fibrosis.
AU Coutelle, Charles; Caplen, Natasha; Hart, Stephen; Huxley, Clare; Williamson, Robert
CS Dep. Biochem. Molecular Genetics, St. Mary's Hosp. Med. Sch., Imperial Coll. London, Norfolk Place, London W2 1PG, UK
SO Archives of Disease in Childhood, (1993) Vol. 68, No. 4, pp. 437-440.
CODEN: ADCHAK. ISSN: 0003-9888.
DT Article
LA English
ED Entered STN: 31 Jul 1993
Last Updated on STN: 31 Jul 1993

L22 ANSWER 41 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:442865 CAPLUS
DN 117:42865
TI Meiotic recombination and segregation of human-derived artificial chromosomes in Saccharomyces cerevisiae
AU Sears, Dorothy D.; Hegemann, Johannes H.; Hieter, Philip
CS Sch. Med., Johns Hopkins Univ., Baltimore, MD, 21205, USA
SO Proceedings of the National Academy of Sciences of the United States of America (***1992***), 89(12), 5296-300
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The authors developed a system that utilizes human DNA-derived yeast artificial chromosomes (YACs) as marker chromosomes to study factors that contribute to the fidelity of meiotic chromosome transmission. Since aneuploidy for the YACs does not affect spore viability, different classes of meiotic missegregation can be scored accurately in four-viable-spore tetrads including precocious sister sepn., meiosis I nondisjunction, meiotic chromatid loss, and meiosis II nondisjunction. Segregation of the homologous pair of 360-kilobase marker YACs was shown to occur with high fidelity in the first meiotic division and was assocd. with a high frequency of recombination within the human DNA segment. By using this exptl. system, a series of YAC deletion derivs. ranging in size from 50 to 225 kilobases was analyzed to directly assess the relationship between meiotic recombination and meiosis I disjunction in a genotypically wild-type background. The relationship between phys. distance and recombination frequency within the human DNA segment was measured to be comparable to that of endogenous yeast chromosomal DNA, ranging from <2.0 to 7.7 kilobases/centimorgan. Phys. anal. of recombinant chromosomes detected no unequal crossing-over at dispersed repetitive elements distributed along the YACs. Recombination between YACs contg. unrelated DNA segments was not obsd. Furthermore, the segregational data indicated that meioses in which YAC pairs failed to recombine exhibited dramatically increased levels of meiosis I missegregation, including both precocious sister chromatid sepn. and nondisjunction.

L22 ANSWER 42 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:564860 CAPLUS
DN 117:164860
TI ***Mammalian*** ***artificial*** ***chromosomes***
AU Brown, William R. A.
CS Oxford Univ., Oxford, UK
SO Current Opinion in Genetics & Development (***1992***), 2(3), 479-86
CODEN: COGDET; ISSN: 0959-437X
DT Journal; General Review
LA English
AB A review with 44 refs. A ***mammalian*** ***artificial*** ***chromosome*** would enable anal. of the cis-acting DNA sequences necessary for mammalian chromosome function and would allow large nos. of genes in a defined sequence environment to be introduced into exptl. animals, agricultural livestock, or human cells. Recent tech. progress suggests that a route to ***mammalian*** ***artificial*** ***chromosome*** construction is now open.

L22 ANSWER 43 OF 44 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:77463 CAPLUS
DN 116:77463
TI The direct screening of cosmid libraries with YAC clones
AU Baxendale, S.; Bates, G. P.; MacDonald, M. E.; Gusella, J. F.; Lehrach, H.
CS Genome Anal. Lab., Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SO Nucleic Acids Research (***1991***), 19(23), 6651
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB YAC clones can be difficult to analyze and manipulate and conversion of a YAC into cosmids provides a useful step in the characterization of the cloned region. Here a method is described for screening cosmid libraries directly with the ***human*** ***artificial*** ***chromosome*** . Two overlapping YAC clones, YGA5 (410 kb) and YGA10 (440 kb), that were isolated from a YAC library constructed from a 48XXXX human cell line, and which lie within the Huntington's disease gene candidate region on 4p16.3 were used. The yeast chromosomes were sepd. by pulsed field gel electrophoresis in LMP agarose (SeaPlaque GTG) and after staining with ethidium bromide, the ***human*** ***artificial*** ***chromosome*** was excised from the gel with the aid of UV irradn. (360 nm). After treatment with Geneclean (BIO 101), the DNA was resuspended in TE to 5 ng/.mu.L. Approx. 50 ng of YAC DNA was labeled by random oligonucleotide priming with 40 .mu.Ci each of [.alpha.-32P]dGTP and [.alpha.-32P]dATP. Repetitive sequences were removed from probes by prehybridization with 1.5 mg/mL of sheared human placental DNA in 0.12 M

Na2HPO4 pH 6.8 for 3 h at 65.degree.. A flow sorted human chromosome 4 cosmid library, contained in 263 microtiter dishes, were spotted in high d. arrays onto Nylon membranes (Hybond N+) using a robotic device. Hybridizations were performed in 50% formamide at 42 degree.. Filters were prehybridized with 100 .mu.g/mL of denatured sonicated human placental DNA for 24 h and then hybridized with probes at a concn. of 106 cpm/mL. The filters were washed and autoradiog. was for 2-3 days. The hybridization of YGA5 and YGA10 to a cosmid filter identified clones consistent with the expected coverage of the library and the size of each YAC insert. This technique allows immediate access to chromosome 4 DNA contained within chimeric YACs and clones contg. 2 artificial chromosomes.

L22 ANSWER 44 OF 44 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on
STN
AN 1988:318292 BIOSIS
DN PREV198835023626; BR35:23626
TI MEGABASE METHODS A QUANTUM JUMP IN RECOMBINANT DNA TECHNIQUES.
AU JORDAN B R [Reprint author]
CS CENTRE D'IMMUNOLOGIE INSERM-CNRS DE MARSEILLE-LUMINY, CASE 906, 13288
MARSEILLE CEDEX 9, FRANCE
SO Bioessays, (1988) Vol. 8, No. 5, pp. 140-145.
CODEN: BIOEEJ. ISSN: 0265-9247.
DT Article
FS BR
LA ENGLISH
ED Entered STN: 11 Jul 1988
Last Updated on STN: 11 Jul 1988

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---Logging off of STN---

=>
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FULL ESTIMATED COST		349.22	349.43

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